

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 5, 2003, 14:26:38 ; Search time 35.3599 Seconds  
(without alignments)  
3196.087 Million cell updates/sec

Title: US-09-854-356-7

Perfect score: 3954

Sequence: 1 MELAALCRWGLLALLPPGA.....GFFCPDPAPGAGMVHRRH 712

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A. Geneseq 15Jun03.\*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.\*  
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.\*  
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.\*  
4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.\*  
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22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.\*  
23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.\*  
24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3954	100.0	712	21	Human HER-2/neu fu
2	3954	100.0	712	23	Her-2/neu extracel
3	3954	100.0	919	21	Human HER-2/neu fu
4	3954	100.0	919	23	Her-2/neu extracel
5	3776	95.5	1200	21	Human HER-2/neu pr
6	3776	95.5	1255	17	HER-2/neu protein.
7	3776	95.5	1255	21	Human HER-2/neu on
8	3776	95.5	1255	21	Human HER-2/neu pr
9	3776	95.5	1255	21	Amino acid sequenc

10	3776	95.5	1255	21	AA192620	Human heregulin 2
11	3776	95.5	1255	22	AAE12130	Human tyrosine kin
12	3776	95.5	1255	22	AAE12130	Human HER-2/neu pr
13	3776	95.5	1255	22	AAE12130	HER2/neu amino aci
14	3776	95.5	1255	22	AAE12130	HER2 transgene pla
15	3776	95.5	1255	23	AAE12130	Human HER-2 protei
16	3776	95.5	1255	23	AAE12130	Human Her2 antigen
17	3776	95.5	1255	23	AAE12130	Human Her-2/neu pr
18	3776	95.5	1255	23	AAE12130	Human Her-2/neu pr
19	3776	95.5	1255	23	AAE12130	Human Her-2/neu on
20	3776	95.5	1255	23	AAU77114	Human HER-2 (erbB2)
21	3776	95.5	1255	23	AAU77114	Breast cancer asso
22	3776	95.5	1255	24	ABR47447	Human Her2/Neu pro
23	3776	95.5	1255	24	ABP74708	Sequence of c-erbB
24	3733	94.4	1433	14	AAE12130	Her2-GM-CSF immuno
25	3632	91.9	782	18	AAE12130	Extracellular HER-
26	3628	91.8	653	21	AAE12130	Human Her-2/neu on
27	3628	91.8	653	23	AAE12130	Human breast cance
28	3606	91.2	1223	23	AAE12130	Human ErbB2 oncopr
29	3590	90.8	645	22	AAE12130	Human ErbB2 extrac
30	3590	90.8	645	23	AAE12130	Human HER2 recepto
31	3590	90.8	645	23	AAE12130	DC8scFv-erbB2EC fu
32	3525	89.2	951	21	AAE12130	Extracellular port
33	3422	86.5	624	11	AAE12130	Mouse Her-2/neu ex
34	3373.5	85.3	920	23	AAE12130	Mouse Her-2/neu ex
35	3373.5	85.3	926	23	AAE12130	Rat Her-2/neu prot
36	3209.5	81.2	1256	21	AAE12130	Rat Her-2/neu onco
37	3209.5	81.2	1256	23	AAE12130	Mouse Her-2/neu pr
38	3189.5	80.7	1256	21	AAE12130	Amino acid sequenc
39	3189.5	80.7	1256	22	AAE12130	Mouse Her-2/neu on
40	3189.5	80.7	1256	23	AAE12130	Rat Her-2/neu prot
41	3110.5	78.7	654	21	AAE12130	Rat Her-2/neu onco
42	3110.5	78.7	654	23	AAE12130	Truncated HER-2, p
43	1827	46.2	420	21	AAE12130	Human p68HER-2 gen
44	1825.5	46.2	419	22	AAE12130	Human truncated HE
45	1824.5	46.1	419	23	AAE12130	

#### ALIGNMENTS

RESULT 1	
AAE12130	
ID	AAE12130 standard; protein; 712 AA.
XX	AAE12130;
AC	AAE12130;
XX	
DT	12-JAN-2001 (first entry)
XX	
DE	Human HER-2/neu fusion protein.
XX	
KW	Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
KW	breast cancer; prostate cancer; ovarian cancer; lung cancer;
KW	colon cancer; fusion protein.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FN	WO200044899-A1.
XX	
PD	03-AUG-2000.
XX	
PF	28-JAN-2000; 2000WO-US02164.
XX	
PR	29-JAN-1999; 98US-0117976.
XX	
PA	(CORI-) CORIXA CORP.
XX	(SMIK) SMITHKLINE BEECHAM.
PI	Cheever MA, Cheysen D;
XX	
DR	WPI; 2000-505976/45.
XX	

HER-2/neu extracellular domain/phosphorylation domain fusion proteins  
 PT useful for vaccinating against breast, ovarian, colon, lung and  
 prostate cancers -

PS Claim 27; Fig 13; 128pp; English.

XX The present sequence is a fusion protein comprising the extracellular  
 CC domain and a preferred portion of the phosphorylation domain of the human  
 CC HER-2/neu protein. HER-2/neu is a member of the tyrosine kinase family of  
 CC receptor-like glycoproteins and shows homology to the epidermal growth  
 CC factor receptor (EGFR). It probably plays a part in cell growth and/or  
 CC differentiation. The HER-2/neu gene is an oncogene. HER-2/neu fusion  
 CC proteins may be used to treat or prevent cancer by eliciting or enhancing  
 CC an immune response to the HER-2/neu protein. They may be used to treat  
 CC malignancies such as breast, ovarian, colon, lung and prostate cancers,  
 CC and may be used as an antigen to vaccinate against these neoplasias.

XX Sequence 712 AA;

SQ Query Match 100.0%; Score 3954; DB 21; Length 712;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-299;  
 Matches 712; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELAALCRWGLLLALLPPGAASSTVCTGTMKRLPASPETHLDMLRHLYQGCVVQGNL 60  
 DB 1 MELAALCRWGLLLALLPPGAASSTVCTGTMKRLPASPETHLDMLRHLYQGCVVQGNL 60

QY 61 ELTYLPTNASLSFLQDIOEVQGVVLAHNOVROVPLQRLIRVGTQOLFEDNALAVLDNG 120  
 DB 61 ELTYLPTNASLSFLQDIOEVQGVVLAHNOVROVPLQRLIRVGTQOLFEDNALAVLDNG 120

QY 121 DPLNNTPTVGTGASPGGLREQLRLSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNQLA 180  
 DB 121 DPLNNTPTVGTGASPGGLREQLRLSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNQLA 180

QY 181 LTLIDNTRACHPCSPMKGSCWGESSEDCOSLRTVTCAGGCARCKGLPTDCCHQC 240  
 DB 181 LTLIDNTRACHPCSPMKGSCWGESSEDCOSLRTVTCAGGCARCKGLPTDCCHQC 240

QY 241 AGCTGPKGSDCLACHFNHSGICELHCPALVTYNTDTFESMPNPGRYTFGASCVTAC 300  
 DB 241 AGCTGPKGSDCLACHFNHSGICELHCPALVTYNTDTFESMPNPGRYTFGASCVTAC 300

QY 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTORCEKSCPKARVCYGLGWEHLREVRVTSAN 360  
 DB 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTORCEKSCPKARVCYGLGWEHLREVRVTSAN 360

QY 361 IQEFAGCKITFGSLAFPLPSFDGDPASNTAPLQEQVFTLEITGYLYISAWPDSL 420  
 DB 361 IQEFAGCKITFGSLAFPLPSFDGDPASNTAPLQEQVFTLEITGYLYISAWPDSL 420

QY 421 DLSVFQNLQVIRGIILHNGAYSTLQGLGTSWLGSLRLSGLSGLALIHNTLHCFVHTV 480  
 DB 421 DLSVFQNLQVIRGIILHNGAYSTLQGLGTSWLGSLRLSGLSGLALIHNTLHCFVHTV 480

QY 481 PWDLFNPHOALLHTANRPEDECVGEGLACHOLCARGHCWGPGTQCVCNCSOFLRGQC 540  
 DB 481 PWDLFNPHOALLHTANRPEDECVGEGLACHOLCARGHCWGPGTQCVCNCSOFLRGQC 540

QY 541 VEECRVLQGLPREYVYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKPPFCVARC 600  
 DB 541 VEECRVLQGLPREYVYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKPPFCVARC 600

QY 601 PSQVKPDLSTYMPITWKPFDDEGACQPCINCHTSCVDLDDKGCFAORASPLTSQNEDLGP 660  
 DB 601 PSQVKPDLSTYMPITWKPFDDEGACQPCINCHTSCVDLDDKGCFAORASPLTSQNEDLGP 660

QY 661 ASPLDSTFYRSLLEDDMGDLVDAEYLYVPQQGFFCFDPAPGAGGMVHRRH 712  
 DB 661 ASPLDSTFYRSLLEDDMGDLVDAEYLYVPQQGFFCFDPAPGAGGMVHRRH 712

AAM51149  
 ID AAM51149 standard; Protein; 712 AA.  
 XX  
 AC AAM51149;  
 XX  
 DT 17-JUN-2002 (first entry)  
 XX  
 DE Her-2/neu extracellular domain-delta-phosphorylation domain fusion.  
 KW Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;  
 KW tyrosine kinase; receptor; c-erbB2; gene therapy.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..653  
 FT Domain /note= "extracellular domain"  
 FT Domain 654..712  
 FT Domain /note= "phosphorylation domain fragment"

WO200212341-A2.  
 14-FEB-2002.  
 03-AUG-2001; 2001WO-US24283.  
 03-AUG-2000; 2000US-0632507.  
 (CORI-) CORIXA CORP.  
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PI Cheever MA, Gheysen D;  
 WIPI; 2002-241743/29.

Her-2/neu fusion protein for treating or preventing cancer by eliciting  
 or enhancing an immune response to the protein, has Her-2/neu  
 extracellular domain fused to Her-2/neu intracellular or  
 phosphorylation domain -

Claim 37; Fig 13; 141pp; English.

The present sequence is that of a fusion protein between the  
 extracellular domain and a fragment (DeltapD) of the phosphorylation  
 domain of human Her-2/neu (see AAM51143), an oncogenic self-protein  
 and target for anti-cancer vaccines. The fusion protein can be  
 obtained by recombinant DNA methods. Her-2/neu overexpression  
 correlates with a poor prognosis in breast and ovarian cancers.  
 The invention provides Her-2/neu fusion proteins, nucleic acids  
 encoding them, viral vectors, and vaccines comprising the fusion  
 proteins or nucleic acid molecules. In preferred fusion proteins,  
 the extracellular domain of Her-2/neu is fused to a Her-2/neu  
 intracellular domain or phosphorylation domain (or its DeltapD  
 fragment). An immune response to Her-2/neu protein is elicited or  
 enhanced by administering the fusion protein in the form of a vaccine,  
 or by transfecting cells of an animal ex vivo with a nucleic acid  
 encoding the fusion protein, and delivering the transfected cells  
 to the animal. The fusion proteins, nucleic acids, and isolated  
 specific T-cells are useful for inhibiting the development of a  
 cancer, especially breast, ovarian, colon, lung or prostate cancer  
 in a patient. T cells that specifically react with a Her-2/neu  
 fusion protein can be used to remove tumour cells from a sample in  
 order to inhibit the development of cancer in a patient.

Query Match 100.0%; Score 3954; DB 23; Length 712;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-299;  
 Matches 712; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELAALCRWGLLLALLPPGAASSTVCTGTMKRLPASPETHLDMLRHLYQGCVVQGNL 60  
 DB 1 MELAALCRWGLLLALLPPGAASSTVCTGTMKRLPASPETHLDMLRHLYQGCVVQGNL 60

QY 61 ELTYLPTNASLFLQDIOEVQGVLIHNOVQVPLQRLRIVRGTQLFEDNVALAVLNG 120  
DB |||||  
DB 61 ELTYLPTNASLFLQDIOEVQGVLIHNOVQVPLQRLRIVRGTQLFEDNVALAVLNG 120  
QY 121 DPLNNTPTVTGASPGGLRELQRLSLEILKGGVLIQVLPOLQYQDTILWKDIFHKNNQLA 180  
DB |||||  
DB 121 DPLNNTPTVTGASPGGLRELQRLSLEILKGGVLIQVLPOLQYQDTILWKDIFHKNNQLA 180  
QY 181 LTLIDTNSRACHPCSPMKGRSGESSEDCQSLTRTVACGACRCKGPLEPTDCCHQC 240  
DB |||||  
DB 181 LTLIDTNSRACHPCSPMKGRSGESSEDCQSLTRTVACGACRCKGPLEPTDCCHQC 240  
QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDFESMPNPEGRYTFGASCVTACP 300  
DB |||||  
DB 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDFESMPNPEGRYTFGASCVTACP 300  
QY 301 YNYLSTDVGSCTLVCPPLHNOVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRVTSAN 360  
DB |||||  
DB 301 YNYLSTDVGSCTLVCPPLHNOVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRVTSAN 360  
QY 361 IOEFAGCKKIFGSLAFPLPESFDGDPASNTAPLOPQLOVFETLEETGYLYISAMPDSL 420  
DB |||||  
DB 361 IOEFAGCKKIFGSLAFPLPESFDGDPASNTAPLOPQLOVFETLEETGYLYISAMPDSL 420  
QY 421 DLSVFQNLQVIRGRILHNGAYSILTLQGLISWGLRSLRELGSGLALIHNTLHLCFVHTV 480  
DB |||||  
DB 421 DLSVFQNLQVIRGRILHNGAYSILTLQGLISWGLRSLRELGSGLALIHNTLHLCFVHTV 480  
QY 481 PWDQLFRNPHQALLHTANRPEDECYVGEGLACHOLCARGHGWGPGTQCVCNCSQFLRGQEC 540  
DB |||||  
DB 481 PWDQLFRNPHQALLHTANRPEDECYVGEGLACHOLCARGHGWGPGTQCVCNCSQFLRGQEC 540  
QY 541 VVECRVLOGLPREYVYNAHCLPCHPECPONGSVTCFGEADOCVACAHYKDPPEFCVAC 600  
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DB 541 VVECRVLOGLPREYVYNAHCLPCHPECPONGSVTCFGEADOCVACAHYKDPPEFCVAC 600  
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DB 601 PSGVKPDLISYMPIWKFPDEEGACQPCINCTHSCVDLDDKGCAPAEORASPLTSQNEIDLGP 660  
QY 661 ASPLDSTFYRSLLEDDMDGLVDAEYLVPOQGFPCDPAPGAGGMVHRRH 712  
DB |||||  
DB 661 ASPLDSTFYRSLLEDDMDGLVDAEYLVPOQGFPCDPAPGAGGMVHRRH 712

## RESULT 3

ID AAB21203  
XX AAB21203 standard; protein; 919 AA.

AC AAB21203;  
XX

DT 12-JAN-2001 (first entry)

XX Human HER-2/neu fusion protein.

XX Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;  
KW breast cancer; prostate cancer; ovarian cancer; lung cancer;  
KW colon cancer; fusion protein.

XX Homo sapiens.  
OS Synthetic.

XX WO200044899-A1.  
PN

PD 03-AUG-2000.

XX 28-JAN-2000; 2000WO-US02164.

XX 29-JAN-1999; 99US-0117976.

XX (CORI-) CORIXA CORP.  
PA (SMIK) SMITHKLINE BEECHAM.

XX Cheever MA, Gheysen D;  
XX WPI; 2000-505976/45.  
XX HER-2/neu extracellular domain/phosphorylation domain fusion proteins  
PT useful for vaccinating against breast, ovarian, colon, lung and  
PT prostate cancers -  
XX  
XX Claim 2; Fig 12; 128pp; English.  
XX The present sequence is a fusion protein comprising the extracellular  
CC domain and the phosphorylation domain of the human HER-2/neu protein.  
CC HER-2/neu is a member of the tyrosine kinase family of receptor-like  
CC glycoproteins and shows homology to the epidermal growth factor receptor  
CC (EGFR). It probably plays a part in cell growth and/or differentiation.  
CC The HER-2/neu gene is an oncogene. HER-2/neu fusion proteins may be used  
CC to treat or prevent cancer by eliciting or enhancing an immune response  
CC to the HER-2/neu protein. They may be used to treat malignancies such as  
CC breast, ovarian, colon, lung and prostate cancers, and may be used as an  
CC antigen to vaccinate against these neoplasias.

XX Sequence 919 AA;  
SQ

Query Match 100.0%; Score 3954; DB 21; Length 919;

Best Local Similarity 100.0%; Pred. No. 6e-299;

Matches 712; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELAALCERWGLLALLPFGAASQVCTGTDKMLRLPASPEHLDMLRHLQSCQVQGNL 60  
DB |||||  
DB 1 MELAALCERWGLLALLPFGAASQVCTGTDKMLRLPASPEHLDMLRHLQSCQVQGNL 60  
QY 61 ELTYLPTNASLFLQDIOEVQGVLIHNOVQVPLQRLRIVRGTQLFEDNVALAVLNG 120  
DB |||||  
DB 61 ELTYLPTNASLFLQDIOEVQGVLIHNOVQVPLQRLRIVRGTQLFEDNVALAVLNG 120  
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DB 121 DPLNNTPTVTGASPGGLRELQRLSLEILKGGVLIQVLPOLQYQDTILWKDIFHKNNQLA 180  
QY 181 LTLIDTNSRACHPCSPMKGRSGESSEDCQSLTRTVACGACRCKGPLEPTDCCHQC 240  
DB |||||  
DB 181 LTLIDTNSRACHPCSPMKGRSGESSEDCQSLTRTVACGACRCKGPLEPTDCCHQC 240  
QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDFESMPNPEGRYTFGASCVTACP 300  
DB |||||  
DB 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDFESMPNPEGRYTFGASCVTACP 300  
QY 301 YNYLSTDVGSCTLVCPPLHNOVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRVTSAN 360  
DB |||||  
DB 301 YNYLSTDVGSCTLVCPPLHNOVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRVTSAN 360  
QY 361 IOEFAGCKKIFGSLAFPLPESFDGDPASNTAPLOPQLOVFETLEETGYLYISAMPDSL 420  
DB |||||  
DB 361 IOEFAGCKKIFGSLAFPLPESFDGDPASNTAPLOPQLOVFETLEETGYLYISAMPDSL 420  
QY 421 DLSVFQNLQVIRGRILHNGAYSILTLQGLISWGLRSLRELGSGLALIHNTLHLCFVHTV 480  
DB |||||  
DB 421 DLSVFQNLQVIRGRILHNGAYSILTLQGLISWGLRSLRELGSGLALIHNTLHLCFVHTV 480  
QY 481 PWDQLFRNPHQALLHTANRPEDECYVGEGLACHOLCARGHGWGPGTQCVCNCSQFLRGQEC 540  
DB |||||  
DB 481 PWDQLFRNPHQALLHTANRPEDECYVGEGLACHOLCARGHGWGPGTQCVCNCSQFLRGQEC 540  
QY 541 VVECRVLOGLPREYVYNAHCLPCHPECPONGSVTCFGEADOCVACAHYKDPPEFCVAC 600  
DB |||||  
DB 541 VVECRVLOGLPREYVYNAHCLPCHPECPONGSVTCFGEADOCVACAHYKDPPEFCVAC 600  
QY 601 PSGVKPDLISYMPIWKFPDEEGACQPCINCTHSCVDLDDKGCAPAEORASPLTSQNEIDLGP 660  
DB |||||  
DB 601 PSGVKPDLISYMPIWKFPDEEGACQPCINCTHSCVDLDDKGCAPAEORASPLTSQNEIDLGP 660  
QY 661 ASPLDSTFYRSLLEDDMDGLVDAEYLVPOQGFPCDPAPGAGGMVHRRH 712

Query Match 100.0%; Score 3954; DB 23; Length 919;  
Best Local Similarity 100.0%; Pred. No. 6e-299;





Best Local Similarity 67.9%; Pred. No. 6.6e-285;		Matches 712; Conservative 0; Mismatches 0; Indels 336; Gaps 1;	
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Db	1	MELALCRWGLLLALLPPGAASQTCTGDMKRLPASPETHLDMRLHLYGQCQVQGNL	60
QY	61	ELTYLPTNASLSFLQDIQEVQGVYLIHNVQVPLQRLRIVRGTLQFEDNYALAVLNG	120
Db	61	ELTYLPTNASLSFLQDIQEVQGVYLIHNVQVPLQRLRIVRGTLQFEDNYALAVLNG	120
QY	121	DPLNNTTPTGASPGRLRLQSLTEILKGVLTORNPOLCYQDTILWKDIFHKNNOLA	180
Db	121	DPLNNTTPTGASPGRLRLQSLTEILKGVLTORNPOLCYQDTILWKDIFHKNNOLA	180
QY	181	LTLIDTNRSRACHPCSPMCKGRCWGESSEDCQSLTRTVACGACRCKGPLPTDCCHQC	240
Db	181	LTLIDTNRSRACHPCSPMCKGRCWGESSEDCQSLTRTVACGACRCKGPLPTDCCHQC	240
QY	241	AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP	300
Db	241	AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP	300
QY	301	YNYLSTDVGSCTLVCPHNFQVTAEDGTQRCCKSPCARVCYGLGMEHLRVRVAVTSAN	360
Db	301	YNYLSTDVGSCTLVCPHNFQVTAEDGTQRCCKSPCARVCYGLGMEHLRVRVAVTSAN	360
QY	361	IOEFAGCKKIFGSLAFPLSPDGSNTAPLQPELOVFETLEITGVLYISAMPDLSL	420
Db	361	IOEFAGCKKIFGSLAFPLSPDGSNTAPLQPELOVFETLEITGVLYISAMPDLSL	420
QY	421	DLVSFQNLQVIRGRILHNGAYSLTLQGLGISWGLSRLSRELGLALIHNTLHLCFVHTV	480
Db	421	DLVSFQNLQVIRGRILHNGAYSLTLQGLGISWGLSRLSRELGLALIHNTLHLCFVHTV	480
QY	481	PWDQLFRNPHQALLHTANRPEDECVEGLACHQLCARGHGWPGTQCVCNCSQFIRGQEC	540
Db	481	PWDQLFRNPHQALLHTANRPEDECVEGLACHQLCARGHGWPGTQCVCNCSQFIRGQEC	540
QY	541	VEECRVLOGLPREYNARHCLCHPECPONGSVTCFGEADQCVACAHYKDPPECVAC	600
Db	541	VEECRVLOGLPREYNARHCLCHPECPONGSVTCFGEADQCVACAHYKDPPECVAC	600
QY	601	PSGVKPDLSYMIWKFPEDEGACQPCINCHTSCVDLDDKGCAPQASPLTS	653
Db	601	PSGVKPDLSYMIWKFPEDEGACQPCINCHTSCVDLDDKGCAPQASPLTS	653
QY	654	-----	653
Db	661	ILLVVLGVVFGILIKRQOKIRKVTMRRLQETELVEPLTPSGAMPNQAQMRILKETEL	720
QY	654	-----	653
Db	721	RKVKVLGSGAFVTVYGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVSP	780
QY	654	-----	653
Db	781	YVSRLLGICLTSTVQLVTLQMPYGCLLDHVRENRLGSLQDLLNWCMIKMSYLEDR	840
QY	654	-----	653
Db	841	LVRDLAARNVLKSPNHVKITDGLARLLDIDETEYHADGKVPKWKMALESILRRFT	900
QY	654	-----	653
Db	901	HQSDVMSYGVTVWELMTFAKPYDGPAREIPDLLEKGERLPQPPICTIDVTYIMVWKCM	960
QY	654	-----	653
Db	961	DNEDLGPASPLDSTFVRSLLDDMDGLVDA	1020
QY	685	BEYLVPOQGFCDPAPGAGGMVHHRH 712	

Db	1021	BEYLVPOQGFCDPAPGAGGMVHHRH	1048
RESULT 8			
AAE21198			
ID	AAE21198	standard; protein; 1255 AA.	
XX			
AC	AAE21198;		
XX			
DT	12-JAN-2001	(first entry)	
XX			
DE	Human HER-2/neu protein.		
XX			
KW	Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;		
KW	breast cancer; prostate cancer; ovarian cancer; lung cancer;		
KW	colon cancer.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200044899-A1.		
XX			
PD	03-AUG-2000.		
XX			
PF	28-JAN-2000; 2000WO-US02164.		
XX			
PR	29-JAN-1999; 99US-0117976.		
XX			
PA	(CORI-) CORIXA CORP.		
PA	(SMIK-) SMITHKLINE BEECHAM.		
XX			
PI	Cheever MA, Gheysen D;		
XX			
DR	WPI; 2000-505976/45.		
DR	N-P8DB; AAA89736.		
XX			
PT	HER-2/neu extracellular domain/phosphorylation domain fusion proteins		
PT	useful for vaccinating against breast, ovarian, colon, lung and		
PT	prostate cancers -		
XX			
PS	Claim 52; Fig 7; 128pp; English.		
CC			
CC	The present sequence is the human HER-2/neu protein. It is a member of		
CC	the tyrosine kinase family of receptor-like glycoproteins and shows		
CC	homology to the epidermal growth factor receptor (EGFR). It probably		
CC	plays a part in cell growth and/or differentiation. The HER-2/neu		
CC	gene is an oncogene. An HER-2/neu fusion protein comprising a		
CC	HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation		
CC	domain may be used to treat or prevent cancer by eliciting or		
CC	enhancing an immune response to the HER-2/neu protein. It may be used		
CC	to treat malignancies such as breast, ovarian, colon, lung and		
CC	prostate cancers, and may be used as an antigen to vaccinate against		
CC	these neoplasias.		
XX			
SQ	Sequence 1255 AA;		
Query Match 95.5%; Score 3776; DB 21; Length 1255;			
Best Local Similarity 67.9%; Pred. No. 6.6e-285;			
Matches 712; Conservative 0; Mismatches 0; Indels 336; Gaps 1;			
QY	1	MELALCRWGLLLALLPPGAASQTCTGDMKRLPASPETHLDMRLHLYGQCQVQGNL	60
Db	1	MELALCRWGLLLALLPPGAASQTCTGDMKRLPASPETHLDMRLHLYGQCQVQGNL	60
QY	61	ELTYLPTNASLSFLQDIQEVQGVYLIHNVQVPLQRLRIVRGTLQFEDNYALAVLNG	120
Db	61	ELTYLPTNASLSFLQDIQEVQGVYLIHNVQVPLQRLRIVRGTLQFEDNYALAVLNG	120
QY	121	DPLNNTTPTGASPGRLRLQSLTEILKGVLTORNPOLCYQDTILWKDIFHKNNOLA	180
Db	121	DPLNNTTPTGASPGRLRLQSLTEILKGVLTORNPOLCYQDTILWKDIFHKNNOLA	180
QY	181	LTLIDTNRSRACHPCSPMCKGRCWGESSEDCQSLTRTVACGACRCKGPLPTDCCHQC	240

181 LTLIDTNRSRACHPCSPMKSGRCWGESSEDCQSLTRIVTCAGGCARCKGLPTDCCHQC 240  
 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDFESMPNPEGRYTFGASCVTACP 300  
 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDFESMPNPEGRYTFGASCVTACP 300  
 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSAN 360  
 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSAN 360  
 361 IOEFAGCKKIFGSLAFPLPSFDGDPASNTAPLQPEQLQVFETLEITGYLISAWPDSL 420  
 361 IOEFAGCKKIFGSLAFPLPSFDGDPASNTAPLQPEQLQVFETLEITGYLISAWPDSL 420  
 421 DLSVFONLQVIRGRILHNGAYSITLQGLGSLWGLRSLRELGLALIHNNHLCFVHTV 480  
 421 DLSVFONLQVIRGRILHNGAYSITLQGLGSLWGLRSLRELGLALIHNNHLCFVHTV 480  
 481 PWDQLFRNPHQALLHTANRPEDECVGEGGLACHQLCARGHCWGPPTQCVNCSQFLRGQBC 540  
 481 PWDQLFRNPHQALLHTANRPEDECVGEGGLACHQLCARGHCWGPPTQCVNCSQFLRGQBC 540  
 541 VBECRVLQGLPREYVNAHCLPCHPCQONGSVTCFGEADQCVACAHYKDPFPCVARC 600  
 541 VBECRVLQGLPREYVNAHCLPCHPCQONGSVTCFGEADQCVACAHYKDPFPCVARC 600  
 601 PSQVKPDLSPYIWKPFDEGACQPCINCTHSCVDLDDKGPACORASPLTS----- 653  
 601 PSQVKPDLSPYIWKPFDEGACQPCINCTHSCVDLDDKGPACORASPLTS----- 653  
 654 ----- 653  
 661 ILLVVVLGVVGLIKERQKIRKTYMRLLQETELVELPTSGAMPNQAMRILKETEL 720  
 654 ----- 653  
 721 RKVKVLGSGAFGVYKGIWIPDGENVKI PVAIKVLENTSPKANKEILDEAYVMAGVGP 780  
 654 ----- 653  
 781 YVRLIGIGICTVQLVQIMPYGLLDHVRNRLGSLQDLINWCMQIAKMSYLEDVR 840  
 654 ----- 653  
 841 LVHRDLAARNVLKSPNHVKITDFGLRLDIDETEHADGGKVPKMWALESLRRRT 900  
 654 ----- 653  
 901 HQSDVMSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPCTTIDVYMIWVKWM 960  
 654 ----- 653  
 961 IDSECRPRFRELVSERFWARDPQRFVITQNEDLGPASPLDSTFYRSLLEDMDGLVDA 1020  
 685 EYLVLPQQGFPCDPAPGAGMVHRRHR 712  
 1021 EYLVLPQQGFPCDPAPGAGMVHRRHR 1048

RESULT 9  
 ID AAY84780  
 ID AAY84780 standard; Protein; 1255 AA.  
 AC AAY84780;  
 DT 08-AUG-2000 (first entry)  
 XX Amino acid sequence of the SPLICE erbB-2 receptor protein.  
 DE SPLICE erbB-2 receptor protein; cell transformation disorder; cancer;  
 XX tumor cell proliferation; tissue degeneration; arthropathy;  
 KW bone resorption; inflammatory disease; degenerative disorder;  
 KW wound healing.

XX Homo sapiens.  
 OS WO200020579-A1.  
 PN 13-APR-2000.  
 PD 01-OCT-1999; 99WO-CA00912.  
 PF 02-OCT-1998; 98US-0165192.  
 PR (UWMC-) UNIV MCMASTER.  
 PA Muller WJ, Siegel PM;  
 PI WPI: 2000-303768/26.  
 DR N-PSDB; AAA14812.  
 XX Nucleic acid encoding an erbB 2 receptor protein designated SPLICE  
 PT erbB-2, inhibitors of the protein are useful for treatment of cancer -  
 PS Claim 3; Fig 2; 60pp; English.  
 XX The present sequence represents a SPLICE erbB-2 receptor protein. The  
 CC protein has an in-frame deletion of 16 amino acids, 2 of which are  
 CC conserved cysteine residues, compared to the unspliced protein. The  
 CC erbB-2 polynucleotide is used to construct probes for detecting  
 CC disorders of cell transformation such as cancer. Antibodies to the  
 CC protein may be used to detect SPLICE erbB-2 in a sample. Agents  
 CC (e.g. antisense oligonucleotides) which inhibit the expression of  
 CC SPLICE erbB-2 are useful for reducing tumor cell proliferation and  
 CC treating cancer. Substances which stimulate SPLICE erbB-2 are useful  
 CC for treating conditions of tissue occurs, such as arthropathy, bone  
 CC resorption, inflammatory diseases, degenerative disorders of the  
 CC central nervous system and wound healing.  
 XX Sequence 1255 AA;

Query Match 95.5%; Score 3776; DB 21; Length 1255;  
 Best Local Similarity 67.9%; Pred. No. 6.e-285; Indels 336; Gaps 1;  
 Matches 712; Conservative 0; Mismatches 0;  
 QY 1 MELAAALRCWGLLALLPFGAASQVCTGDMKRLPASPETHLDMRLHLYQGCQVQGNL 60  
 DB 1 MELAAALRCWGLLALLPFGAASQVCTGDMKRLPASPETHLDMRLHLYQGCQVQGNL 60  
 QY 61 ELTYLPTNASLSFLQDIQEVQYVLIHNRQVPLQRLRIVRGTLFEDNYALAVLNG 120  
 DB 61 ELTYLPTNASLSFLQDIQEVQYVLIHNRQVPLQRLRIVRGTLFEDNYALAVLNG 120  
 QY 121 DPLNNTTPTVGTASPGGLRELQRLSLEILKGVLIQRNPOLCYQDTILWKDIFHKNNQLA 180  
 DB 121 DPLNNTTPTVGTASPGGLRELQRLSLEILKGVLIQRNPOLCYQDTILWKDIFHKNNQLA 180  
 QY 181 LTLIDTNRSRACHPCSPMKSGRCWGESSEDCQSLTRIVTCAGGCARCKGLPTDCCHQC 240  
 DB 181 LTLIDTNRSRACHPCSPMKSGRCWGESSEDCQSLTRIVTCAGGCARCKGLPTDCCHQC 240  
 QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDFESMPNPEGRYTFGASCVTACP 300  
 DB 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDFESMPNPEGRYTFGASCVTACP 300  
 QY 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSAN 360  
 DB 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSAN 360  
 QY 361 IOEFAGCKKIFGSLAFPLPSFDGDPASNTAPLQPEQLQVFETLEITGYLISAWPDSL 420  
 DB 361 IOEFAGCKKIFGSLAFPLPSFDGDPASNTAPLQPEQLQVFETLEITGYLISAWPDSL 420  
 QY 421 DLSVFONLQVIRGRILHNGAYSITLQGLGSLWGLRSLRELGLALIHNNHLCFVHTV 480

```
Db 421 DLSVFQNLQVIRGRILHNGAYSLSLTQLGLGISWLGRLSRLSRLSGLALIHNNTHLCFVHTV 480
QY 481 PWDQLFRNPHQALLHTANRPEDECVCVEGLACHQLCARGHCWGPPTQCVCNCSQFLRGQEC 540
Db 481 PWDQLFRNPHQALLHTANRPEDECVCVEGLACHQLCARGHCWGPPTQCVCNCSQFLRGQEC 540
QY 541 VBECRVLQGLPREYNARHCLCHPECPQNGSVTCFGEADQCACAHYKDPPEFCVARC 600
Db 541 VBECRVLQGLPREYNARHCLCHPECPQNGSVTCFGEADQCACAHYKDPPEFCVARC 600
QY 601 PSGVKPDLSPYMPKFPDEEGACQPCINCHTSCVDLDDKGPABORASPLTS ----- 653
Db 601 PSGVKPDLSPYMPKFPDEEGACQPCINCHTSCVDLDDKGPABORASPLTSIISAVVG 660
QY 654 ----- 653
Db 661 ILLVVVLGVVFGILIKRROQKIRKYTMRLLOETELVEPLTPSGAMPNQAQMRILKETEL 720
QY 654 ----- 653
Db 721 RKVKVLGSGAGCTVYKGIWPDGENVKIPVAIKVLRENTSPKANKEILDYATVMAGVGP 780
QY 654 ----- 653
Db 781 YVSRLLGICLTSTVQLVTLQMPYGCLLDHVRENRRGLSGQDLLNWMQIAKMSYLEVDVR 840
QY 654 ----- 653
Db 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGKGVPKWMALLESILRRFT 900
QY 654 ----- 653
Db 901 HQSDVMSYGVTVWELMTFCAKPYDGPAREIPDLLEKGERLPQPPICTIDVVMIMVKCWM 960
QY 654 ----- QNEDLGASPLDSTFYRSILLEDDMDGLVDA 684
Db 961 IDSECRPRFELVSFERSWARDPQRFVQIQLDGLPASPLDSTFYRSILLEDDMDGLVDA 1020
QY 685 EBYLVPQGGFFCDPAPGAGGMVHRHR 712
Db 1021 EBYLVPQGGFFCDPAPGAGGMVHRHR 1048

RESULT 10
ID AAY92620
XX AAY92620 standard; Protein; 1255 AA.
AC AAY92620;
XX
XX 10-AUG-2000 (first entry)
XX
DE Human heregulin 2 (Her2).
XX
KW Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity;
KW self-protein; cancer; breast cancer; prostate cancer;
KW cell-associated peptide antigen; foreign epitope.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..173
FT /label= N-terminal
FT /note= "mature polypeptide"
FT Region 5..25
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Region 59..73
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Region 103..117
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Region 149..163
```

```
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Domain 174..323
FT /label= Cysteine_rich_domain
FT Region 210..224
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Region 250..264
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Domain 324..483
FT /label= Ligand_binding_domain
FT Region 325..339
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Region 369..383
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Region 465..479
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Domain 484..623
FT /label= Cysteine_rich_domain
FT Region 579..593
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Domain 624..654
FT /label= Transmembrane_domain
FT Region 632..652
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Region 653..667
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Domain 655..1010
FT /label= Tyrosine_kinase_domain
FT Region 661..675
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Region 695..709
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Region 710..730
FT /label= insertion_region
FT /note= "suitable for foreign epitope insertion"
FT Domain 1011..1235
FT /label= C-terminal_domain
XX
XX WO200020027-A2.
XX PD 13-APR-2000.
XX
XX 05-OCT-1999; 99WO-DK00525.
XX
XX 05-OCT-1998; 98DK-0001261.
XX PR 20-OCT-1998; 98US-0105011.
XX
XX (MEBI-) M & E BIOTECH AS.
XX
XX Steinaa L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;
XX Gautam A, Birk P, Karlsson G;
XX
XX WPI; 2000-349917/30.
XX DR N-PSDB; AAA09455.
XX
XX Inducing immune responses to weakly immunogenic, tumor associated
XX peptide antigens for the treatment of breast and prostate cancer
XX
XX Claim 62; Page 193-198; 220pp; English.
XX
XX This is the human heregulin 2 (Her2) sequence. Immunogenic analogues of
XX Her2 can be used in the claimed method as an autovaccine to induce a CTL
XX response. Subdominant CTL epitopes, antibody binding regions and
```

CC Cysteine residues involved in disulfide bonds are preserved in the  
CC immunogenized forms. Regions suitable for the insertion of foreign T  
CC helper epitopes were identified (see features table). The method  
CC is used for inducing immune responses against weakly immunogenic  
CC cell-associated peptide antigens (PA) such as those associated with  
CC cancers (self-proteins), e.g. human prostate specific membrane antigen  
CC (PSM), hergulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b).  
CC The method comprises effecting simultaneous presentation by antigen  
CC producing cells (APCs) of the animals immune system of: (1) at least 1  
CC CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1  
CC B-cell group derived from the cell-associated PA; and (2) at least 1  
CC first T helper cell group from which is foreign to the animal. Analogues of  
CC human PSM, human Her2 and human/murine FGF8b comprising a substantial  
CC part of all known and predicted CTL and B-cell epitopes of the respective  
CC PA and including at least one foreign T helper epitope are also claimed.  
CC The method is used to treat prostate, prostate/breast or breast cancer  
CC when the PA is human PSM, FGF8b and Her2, respectively.  
XX  
SQ Sequence 1255 AA;  
Query Match 95.5%; Score 3776; DB 21; Length 1255;  
Best Local Similarity 67.9%; Pred. No. 6.6e-285;  
Matches 712; Conservative 0; Mismatches 0; Indels 336; Gaps 1;  
QY 1 MELAALCRWGLLIALLPPGAASQTCTGDMKRLRASPETHLDMLRHLRYQCGVQVQNL 60  
DB 1 MELAALCRWGLLIALLPPGAASQTCTGDMKRLRASPETHLDMLRHLRYQCGVQVQNL 60  
QY 61 ELTYLPTNASLSFLDIOEVQGVVLAHQVQVPLRIRIVRGTLFEDNYALAVLDNG 120  
DB 61 ELTYLPTNASLSFLDIOEVQGVVLAHQVQVPLRIRIVRGTLFEDNYALAVLDNG 120  
QY 121 DPLNNTPTVGTASPGGLRELRLSLTEILKGGVLIQRPOLQCYQDTILWKDIFHKNNQLA 180  
DB 121 DPLNNTPTVGTASPGGLRELRLSLTEILKGGVLIQRPOLQCYQDTILWKDIFHKNNQLA 180  
QY 181 LTLIDTNRGRACHPCSPMKGSRGWESSEDCQSLTRTVAGCARCKGLPTDCHEQC 240  
DB 181 LTLIDTNRGRACHPCSPMKGSRGWESSEDCQSLTRTVAGCARCKGLPTDCHEQC 240  
QY 241 AAGCTGPKHSDCLACLFHNSGTCELHCPALVTYNTDFESMPNREGYTFGASCVTACP 300  
DB 241 AAGCTGPKHSDCLACLFHNSGTCELHCPALVTYNTDFESMPNREGYTFGASCVTACP 300  
QY 301 YNVLSTDVGSCTLVCPHLNQEVTAEDGTORCEKSKPCARVCYGLGMEHLREVRAVTSAN 360  
DB 301 YNVLSTDVGSCTLVCPHLNQEVTAEDGTORCEKSKPCARVCYGLGMEHLREVRAVTSAN 360  
QY 361 IQEFACKKIFGSLAFPLPSFDGDPASNTAPLOPEQLQVFETLEETGYLYISAMPDSL 420  
DB 361 IQEFACKKIFGSLAFPLPSFDGDPASNTAPLOPEQLQVFETLEETGYLYISAMPDSL 420  
QY 421 DLSVFQNLQVIRGRILHNGAYSITLOGLGISWGLSLRSLGSLALIHNTHLCEVHTV 480  
DB 421 DLSVFQNLQVIRGRILHNGAYSITLOGLGISWGLSLRSLGSLALIHNTHLCEVHTV 480  
QY 481 PDQLFRNPHOALLHTANRDEDCVCEGLACHQLCARGHCWGPGTQCVNCSQFARGQEC 540  
DB 481 PDQLFRNPHOALLHTANRDEDCVCEGLACHQLCARGHCWGPGTQCVNCSQFARGQEC 540  
QY 541 VEECRVLQGLPREYVNAHCLPCHPCQPONGSVTCFGEADQCVACAHYKPPFCVARC 600  
DB 541 VEECRVLQGLPREYVNAHCLPCHPCQPONGSVTCFGEADQCVACAHYKPPFCVARC 600  
QY 601 PSGVKPDLSYMPYWKPFDEGACQPCPINCTHSCVDLDDKGCFAEORASPLTS ----- 653  
DB 601 PSGVKPDLSYMPYWKPFDEGACQPCPINCTHSCVDLDDKGCFAEORASPLTSIVSAVVG 660  
QY 654 ----- 653  
DB 661 ILLVVVLGVVFGILIKRQOKIRKTYMRRLLQETELVEPLTPSGAMPNQAMRILKETEL 720  
QY 654 ----- 653

DB 721 RKVKVLGSGARFTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVSP 780  
QY 654 ----- 653  
DB 781 YVSRILGICLTSTVQLVTQMLPYGCLLDHVRENRLGSLQDLNWCMIKAGMSYLEVDR 840  
QY 654 ----- 653  
DB 841 LVHRDLAARNVLKSPNHNKIDTDFGLARLLDIDETEHADGKVPKIKWALESLIRRRPT 900  
QY 654 ----- 653  
DB 901 HQSDVWSYGVTVWELMTFGAKPYDGI PAREIPDLLEKGERLPQPPICITIDVYIMVWKWM 960  
QY 654 ----- QNEDLGSPASPLDSTFYRSLEDDDDMGDLVDA 684  
DB 961 IDSECRPRFRELVSERFMRDPPQRFVVIQNEEDLGSPASPLDSTFYRSLEDDDDMGDLVDA 1020  
QY 685 BEYLVPQGGFFCPDPAPGAGGMVHRHR 712  
DB 1021 BEYLVPQGGFFCPDPAPGAGGMVHRHR 1048  
RESULT 11  
ID AA012130 standard; Protein; 1255 AA.  
XX AA012130;  
XX 18-DEC-2001 (first entry)  
XX Human tyrosine kinase-type receptor, HER-2.  
XX Therapeutic compound; major histocompatibility complex; vaccine;  
KW antigenic peptide; MHC; immunoregulatory; immune response; HER-2;  
KW adoptive immunotherapy; anti-cancer; breast cancer antigen; APC;  
KW antigen presenting cell; human; tyrosine kinase-type receptor.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH Region 774..782  
FT /note= "Antigenic epitope"  
XX WO200168677-A2.  
XX 20-SEP-2001.  
XX 16-MAR-2001; 2001WO-US40328.  
XX 16-MAR-2000; 2000US-0527487.  
XX (GENZ ) GENZYME CORP.  
XX Nicolette CA;  
XX WPI; 2001-616284/71.  
XX N-PSDB; AAD19731.  
XX Novel synthetic therapeutic compound for inducing immune response and  
PT for use in adoptive immunotherapy, has enhanced binding to major  
PT histocompatibility molecules and enhanced immunoregulatory properties  
PT  
XX Claim 4; Page 63-67; 69pp; English.  
XX The invention relates to synthetic therapeutic compounds (antigenic  
CC peptides) with enhanced binding to major histocompatibility complex  
CC (MHC) molecules and enhanced immunoregulatory properties relative  
CC to their natural counterparts. Compounds of the invention are useful  
CC for inducing an immune response in a subject and for use in adoptive  
CC immunotherapy. They are useful as components of anti-cancer vaccines

CC and to expand immune effector cells that are specific for cancers  
CC characterised by expression of the breast cancer antigen, HER-2.  
CC Polynucleotides that encode peptides of the invention are useful as  
CC hybridisation probes and as primers for the detection of genes of gene  
CC transcripts that are expressed in antigen presenting cells (APCs), to  
CC confirm transduction of polynucleotides into host cells. The present  
CC sequence is human tyrosine kinase-type receptor, HER-2. Compounds  
CC of the invention are designed based on the HER-2 antigenic peptide  
XX (774-782).  
XX  
SQ Sequence 1255 AA;  
Query Match 95.5%; Score 3776; DB 22; Length 1255;  
Best Local Similarity 67.9%; Pred. No. 6.6e-285;  
Matches 712; Conservative 0; Mismatches 0; Indels 336; Gaps 1;  
QY 1 MELAALCRWGLLLALLPPGAASVCTGTDMLRLPASPEHDLMLRLHYGCGVQGNL 60  
DB 1 MELAALCRWGLLLALLPPGAASVCTGTDMLRLPASPEHDLMLRLHYGCGVQGNL 60  
QY 61 ELTYLPTNASLFLQDIQEVQGVLIHNOVRQVPLQRLRIVRGTQLFEDNYALVLDNG 120  
DB 61 ELTYLPTNASLFLQDIQEVQGVLIHNOVRQVPLQRLRIVRGTQLFEDNYALVLDNG 120  
QY 121 DPLNNTPTVTGASPGGLRELQRLSRLTEILKGVLIQRPOLCYQDTILWKDIFHKNOLA 180  
DB 121 DPLNNTPTVTGASPGGLRELQRLSRLTEILKGVLIQRPOLCYQDTILWKDIFHKNOLA 180  
QY 181 LTLIDTNSRACHPCSPCKGSRGCESEDCOSLTRTVCAGGCARCKGPLTDCCHQC 240  
DB 181 LTLIDTNSRACHPCSPCKGSRGCESEDCOSLTRTVCAGGCARCKGPLTDCCHQC 240  
QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTPESMPNPEGRYTFGASCVTACP 300  
DB 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTPESMPNPEGRYTFGASCVTACP 300  
QY 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVAVTSAN 360  
DB 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVAVTSAN 360  
QY 361 IQEFAGCKIFGSLAFPLSPFGDPASNTAPLOPQLQVFEITLITGYLISAWPDSL 420  
DB 361 IQEFAGCKIFGSLAFPLSPFGDPASNTAPLOPQLQVFEITLITGYLISAWPDSL 420  
QY 421 DLSVFQNLQVIRGRILHNGAYSILTLQGLISWGLSLRELGLALHNTLHLCFVHTV 480  
DB 421 DLSVFQNLQVIRGRILHNGAYSILTLQGLISWGLSLRELGLALHNTLHLCFVHTV 480  
QY 481 PWDQLFRNPHQALLHTANRPEDECVGEGGLACHQLCARGHCWGPPTQCVNCSQFLRGQEC 540  
DB 481 PWDQLFRNPHQALLHTANRPEDECVGEGGLACHQLCARGHCWGPPTQCVNCSQFLRGQEC 540  
QY 541 VZECRVLOGLPREYNARHCLCHPECPQNGSVTCFGEADQCVACAHYKDPFPCVARC 600  
DB 541 VZECRVLOGLPREYNARHCLCHPECPQNGSVTCFGEADQCVACAHYKDPFPCVARC 600  
QY 601 PSGVXPDLISYMPIWKPFPDEGACQPCINCTHSCVDLDDKGPASORASPLTS ----- 653  
DB 601 PSGVXPDLISYMPIWKPFPDEGACQPCINCTHSCVDLDDKGPASORASPLTSIVSAVVG 660  
QY 654 ----- 653  
DB 661 ILLVVVLGVVFGILIKRQOKIRKYTMRELLQETELVEPLTPSGAMPNQAQMRILKETEL 720  
QY 654 ----- 653  
DB 721 RKVKVLGSGAFGVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYMWAGVSP 780  
QY 654 ----- 653  
DB 781 YVSRLLGICLTSTVLQVLTQMLPYGCLLDHVRNRRGLSGQDILLNMCMIAGMSYLEVDR 840  
QY 654 ----- 653

DB 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGGKVPKIMMALESILRRRT 900  
QY 654 ----- 653  
DB 901 HQSDVWSYGVTVWELMTFGAXPYDGIPIAREIPDLLEKGERLPQPPICTIDYVMINVKWM 960  
QY 654 -----QNEGLGPASPLDSTFYRSLLEDDMDGLVDA 684  
DB 961 IDSECRPRFRELVSFESRMARDPQRFVVIQNEGLGPASPLDSTFYRSLLEDDMDGLVDA 1020  
QY 685 BEYLVPQGGFFCPDPAPGAGGMVHRHR 712  
DB 1021 BEYLVPQGGFFCPDPAPGAGGMVHRHR 1048  
RESULT 12  
AAB85458  
ID AAB85458 standard; Protein; 1255 AA.  
XX  
AC AAB85458;  
DT 25-SEP-2001 (first entry)  
XX  
DE Human HER-2/neu protein.  
XX  
KW Antigen-presenting cell; immunogenic; immune response; HER-2/neu;  
KW oncogene; cancer; cytostatic; vaccine; p185; c-erbB2.  
XX  
OS Homo sapiens.  
XX  
PN WO200153463-A2.  
PD 26-JUL-2001.  
XX  
PF 19-JAN-2001; 2001WO-US01850.  
PR 21-JAN-2000; 2000US-0177545.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Cheever MA, Hand-Zimmermann S;  
XX  
DR WPI; 2001-476112/51.  
DR N-PSDB; AAH23392.  
XX  
PT New antigen-presenting cells, useful as vaccines for eliciting or  
PT enhancing an immune response to HER-2/neu protein, particularly useful  
PT for treating or preventing cancer, e.g. breast cancer -  
XX  
PS Claim 2; Page 41-46; 49pp; English.  
XX  
CC The invention provides an isolated antigen-presenting cell, which  
CC expresses at least an immunogenic portion of a polypeptide that produces  
CC an immune response to HER-2/neu protein. The antigen-presenting cells are  
CC useful as vaccines for eliciting or enhancing an immune response to  
CC HER-2/neu protein, particularly in treating or preventing malignancies in  
CC which the HER-2/neu oncogene is associated. Specifically, these are  
CC useful for treating or preventing cancer, e.g. breast cancer, ovarian,  
CC colon, lung or prostate cancers. The present sequence represents  
CC the human HER-2/neu protein (also known as p185 or c-erbB2).  
XX  
SQ Sequence 1255 AA;  
Query Match 95.5%; Score 3776; DB 22; Length 1255;  
Best Local Similarity 67.9%; Pred. No. 6.6e-285;  
Matches 712; Conservative 0; Mismatches 0; Indels 336; Gaps 1;  
QY 1 MELAALCRWGLLLALLPPGAASVCTGTDMLRLPASPEHDLMLRLHYGCGVQGNL 60  
DB 1 MELAALCRWGLLLALLPPGAASVCTGTDMLRLPASPEHDLMLRLHYGCGVQGNL 60  
QY 61 ELTYLPTNASLFLQDIQEVQGVLIHNOVRQVPLQRLRIVRGTQLFEDNYALVLDNG 120



Db 121 DPLNNTPTVTGASPGRLRLQRLSLTEILKGGVLIQRPOLCYQDTILWKDIFHKNNQLA 180  
QY 181 LTLIDTNRACHPCSPMKCGSRWGSEDCOSLTRTVCAGGCARCKGPLEPTDCCHEQC 240  
Db 181 LTLIDTNRACHPCSPMKCGSRWGSEDCOSLTRTVCAGGCARCKGPLEPTDCCHEQC 240  
QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300  
Db 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300  
QY 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTORCEKSKPCARVCYGLGMHLREVRVTSAN 360  
Db 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTORCEKSKPCARVCYGLGMHLREVRVTSAN 360  
QY 361 IOEFAGCKKIFGSLAFLPESFDGDPASNTAPLOPEQLQVFETLEEITGYLISAWPDSL 420  
Db 361 IOEFAGCKKIFGSLAFLPESFDGDPASNTAPLOPEQLQVFETLEEITGYLISAWPDSL 420  
QY 421 DLSVFQNLQVIRGRILHNGAYSILTLQGLGISWLGRLSRLGSLALIHNNTHLCFVHTV 480  
Db 421 DLSVFQNLQVIRGRILHNGAYSILTLQGLGISWLGRLSRLGSLALIHNNTHLCFVHTV 480  
QY 481 PNDQLFRNPHQALLHTANRPEDECVEGGLACHQLCARGHCWGPPTQCVCNCSQFLRGQC 540  
Db 481 PNDQLFRNPHQALLHTANRPEDECVEGGLACHQLCARGHCWGPPTQCVCNCSQFLRGQC 540  
QY 541 VBECRVLQGLPREYVNAHCLPCHPCQPQNGSVTCFGEADQCVACAHYKDPFPFCVAPC 600  
Db 541 VBECRVLQGLPREYVNAHCLPCHPCQPQNGSVTCFGEADQCVACAHYKDPFPFCVAPC 600  
QY 601 PSQVPRDLSPYPIWKFPEDEGACQPCINCTHSCVDLDDKGCFAEQASPLTS----- 653  
Db 601 PSQVPRDLSPYPIWKFPEDEGACQPCINCTHSCVDLDDKGCFAEQASPLTSIIISAVVG 660  
QY 654 ----- 653  
Db 661 ILLVVLGVVFGILIKRQOKIRKYTMRLRLQETELVEPLTPSGAMPNQAQMRILKTEL 720  
QY 654 ----- 653  
Db 721 RKVKVLGSCAGTVYKGIWIPDGENVKIPVALKVLRENTSPKANKEILDEATVMAGVSP 780  
QY 654 ----- 653  
Db 781 YVSRLLGICLTSTVLQVLTQMPYGLLDHVRNRLGSLQDLNNWCMIKAGMSYLEVDVR 840  
QY 654 ----- 653  
Db 841 LVHRLAARNVLKSPNHVKITDFGLARLLDIDETEHADGGKVPKWMALLESILRRRPT 900  
QY 654 ----- 653  
Db 901 HOSDWSYGVTVWELMTFGAKPYDGIPIAREIPDLLEKGERLPQPICTIDVYIMVWKCM 960  
QY 654 -----QNEDLGPASPLDSTFYRSLLLEDDMDGDLVDA 684  
Db 961 IDSECRPRELVSFSRWARDPPQFVVITQNEDLGPASPLDSTFYRSLLLEDDMDGDLVDA 1020  
QY 685 EBYLVPQOGFFCPDPAPGAGMVHRRH 712  
Db 1021 EBYLVPQOGFFCPDPAPGAGMVHRRH 1048

RESULT 14

AAB60167

ID AAB60167 standard; Protein; 1255 AA.

XX

AC AAB60167;

XX

DT 03-APR-2001 (first entry)

XX

DE HER2 transgene plasmid construct encoded protein.

XX Human; HER2; ErbB2 receptor; p185neu; maytansinoid conjugate; cancer;  
KW antibody.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200100244-A2.  
XX PD 04-JAN-2001.  
XX 23-JUN-2000; 2000WO-US17229.  
XX 25-JUN-1999; 99US-0141316.  
PR 16-MAR-2000; 2000US-0189844.  
XX (GETH ) GENENTECH INC.  
PI Erickson S, Schwall R;  
XX WPI; 2001-061962/07.  
DR N-PSDB; AAF24297.  
XX Treating tumors, particularly breast cancers, which overexpress an ErbB  
PT receptor and does not respond to an anti-ErbB antibody, comprises  
PT conjugating the antibody to a maytansinoid -  
XX Example 3; Fig 4; 92pp; English.  
PS The present invention provides a method of treating cancer by  
CC administering a conjugate of anti-ErbB antibody with a maytansinoid. In  
CC particular, the antibody is directed against ErbB2 (also known as HER2  
CC and p185neu). The method is particularly useful in the treatment of  
CC breast, ovarian, stomach, endometrial, salivary gland, lung, kidney,  
CC colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.  
XX SQ Sequence 1255 AA;

Query Match 95.5%; Score 3776; DB 22; Length 1255;  
Best Local Similarity 67.9%; Pred. No. 6, 6e-285;  
Matches 712; Conservative 0; Mismatches 0; Indels 336; Gaps 1;  
QY 1 MELAALCRWGLLLALLPPGAASVCTCTDMKRLPASPETHLDMRLHYQCQVQGNL 60  
Db 1 MELAALCRWGLLLALLPPGAASVCTCTDMKRLPASPETHLDMRLHYQCQVQGNL 60  
QY 61 ELTYLPTNASLSPFDIOEVQGVLIHNVQRPVLPQRLRVGRQTQLPEDNYALAVLNG 120  
Db 61 ELTYLPTNASLSPFDIOEVQGVLIHNVQRPVLPQRLRVGRQTQLPEDNYALAVLNG 120  
QY 121 DPLNNTPTVTGASPGRLRLQRLSLTEILKGGVLIQRPOLCYQDTILWKDIFHKNNOLA 180  
Db 121 DPLNNTPTVTGASPGRLRLQRLSLTEILKGGVLIQRPOLCYQDTILWKDIFHKNNOLA 180  
QY 181 LTLIDTNRACHPCSPMKCGSRWGSEDCOSLTRTVCAGGCARCKGPLEPTDCCHEQC 240  
Db 181 LTLIDTNRACHPCSPMKCGSRWGSEDCOSLTRTVCAGGCARCKGPLEPTDCCHEQC 240  
QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300  
Db 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300  
QY 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTORCEKSKPCARVCYGLGMHLREVRVTSAN 360  
Db 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTORCEKSKPCARVCYGLGMHLREVRVTSAN 360  
QY 361 IOEFAGCKKIFGSLAFLPESFDGDPASNTAPLOPEQLQVFETLEEITGYLISAWPDSL 420  
Db 361 IOEFAGCKKIFGSLAFLPESFDGDPASNTAPLOPEQLQVFETLEEITGYLISAWPDSL 420  
QY 421 DLSVFQNLQVIRGRILHNGAYSILTLQGLGISWLGRLSRLGSLALIHNNTHLCFVHTV 480  
Db 421 DLSVFQNLQVIRGRILHNGAYSILTLQGLGISWLGRLSRLGSLALIHNNTHLCFVHTV 480

QY 481 PWDQFRNPHOALLHTANRPEDECEVGEGLACHOLCARGHCWGPGPTQCVCNCSQFLRGQEC 540  
DB 481 PWDQFRNPHOALLHTANRPEDECEVGEGLACHOLCARGHCWGPGPTQCVCNCSQFLRGQEC 540  
QY 541 VEECRVLQGLPREYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKDPFPCVARC 600  
DB 541 VEECRVLQGLPREYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKDPFPCVARC 600  
QY 601 PSQVKPDLSPYMPKPPDEGACQPCPINCTHSCVDLDDKGCAPAEORASPLTS 653  
DB 601 PSQVKPDLSPYMPKPPDEGACQPCPINCTHSCVDLDDKGCAPAEORASPLTSIVSAVVG 660  
QY 654 654 653  
DB 661 ILLVVVLGVVFGILIKRQOKIRKYMRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720  
QY 654 654 653  
DB 721 RKVKVLGSGAGFTVYKGIWIPDGENVKIPVAIKVLRNTSPKANKELDEAYVMAGVGS 780  
QY 654 654 653  
DB 781 YVSRLLGICLTSTVQLVTLQMPYGCCLLDHVRENRLGSLQDILLNWCWIAKGMYSLE 840  
QY 654 654 653  
DB 841 LVHRDLAARNVLVKSNNHVKITPGLARLLDIDETEHADGGKVPKVMMALESILRRRT 900  
QY 654 654 653  
DB 901 HQSDVMSYGVTVWELMTFGAKPYDIPAREIPDLEKGERLPQPPICITIDVYIMVKCW 960  
QY 654 654 653  
DB 961 IDSECRPRFRELVSFERSWARDPQRFVIONEDLGPASPLDSTFYRSLLDDMDGLVDA 1020  
QY 685 EYLVVPOQGFCDPAPGAGMVHRRH 712  
DB 1021 EYLVVPOQGFCDPAPGAGMVHRRH 1048

RESULT 15  
AAE26349  
ID AAE26349 standard; Protein; 1255 AA.  
XX AC AAE26349;  
DT 13-DEC-2002 (first entry)  
DE Human HER-2 protein.  
XX Transgenic animal; transgenic; mammary gland cell; HER2; tumour;  
KW cancer; therapy; apoptosis; cytostatic; human.  
XX Homo sapiens.  
XX US2002035736-A1.  
XX 21-MAR-2002.  
XX 16-MAR-2001; 2001US-0811115.  
XX 16-MAR-2000; 2000US-189844P.  
XX (ERIC/) ERICKSON S.  
PA (KING/) KING K.  
PA (SCHW/) SCHWALL R.  
XX Erickson S, King K, Schwall R;  
PI WPI; 2002-401155/43.  
DR N-PSDB; AAD43934, AAD43935.

XX New transgenic non-human mammal that produces detectable levels of a  
PT native human HER2 protein in its mammary gland cells, useful as tumor  
PT models for testing HER2-directed cancer therapies, and for identifying  
PT anticancer agents  
XX Example 2; Page 26-29; 83pp; English.  
XX The invention relates to a transgenic non-human mammal that produces in  
CC its mammary gland cells detectable levels of a native human HER2 protein  
CC or its fragment. The transgenic animals are useful as tumor models for  
CC testing HER2-directed cancer therapies, and for identifying anticancer  
CC agents. The animals may also be used as source of cells which can be  
CC immortalised in culture, in screening for compounds that have potential  
CC as prophylactic or therapeutic treatments of diseases or disorders  
CC involving expression of HER2. The anti-cancer molecules are useful for  
CC inducing apoptosis or cell death of cancer cells. The present sequence  
CC is human HER-2 protein.  
XX Sequence 1255 AA;  
QY Query Match 95.5%; Score 3776; DB 23; Length 1255;  
Best Local Similarity 67.9%; Pred. No. 6.6e-285;  
Matches 712; Conservative 0; Mismatches 0; Indels 336; Gaps 1;  
QY 1 MELAALCRWGLLLALLPFGAASQVCTGDMKRLPASPETHLDMRLHLYQCGVQVQGNL 60  
DB 1 MELAALCRWGLLLALLPFGAASQVCTGDMKRLPASPETHLDMRLHLYQCGVQVQGNL 60  
QY 61 ELYLPTNASLFLQDIQEVQGVLIANQVRQVPLRLRIVRGTLQFEDNVALAVLNG 120  
DB 61 ELYLPTNASLFLQDIQEVQGVLIANQVRQVPLRLRIVRGTLQFEDNVALAVLNG 120  
QY 121 DPLNNTPTVGTASPGGLRELQRLSLEILKGVLIQORNPOLCVQDTILWKDIFHKNQLA 180  
DB 121 DPLNNTPTVGTASPGGLRELQRLSLEILKGVLIQORNPOLCVQDTILWKDIFHKNQLA 180  
QY 181 LTLIDTNRSRACHPCSPMKSGRCSSEDCQSLTRTVACGCGARCKGPLPTDCCHQC 240  
DB 181 LTLIDTNRSRACHPCSPMKSGRCSSEDCQSLTRTVACGCGARCKGPLPTDCCHQC 240  
QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTAC 300  
DB 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTAC 300  
QY 301 YNYLSTDVGSCTLVCPHNOEVTADGTQRCCKSPCARVCYGLGMEHLREVAVTSAN 360  
DB 301 YNYLSTDVGSCTLVCPHNOEVTADGTQRCCKSPCARVCYGLGMEHLREVAVTSAN 360  
QY 361 IOEFAGCKKI FGS LAF LPE SFDGDPASNTAPLPQLOLVFETLEITGYLYISAWPDSL 420  
DB 361 IOEFAGCKKI FGS LAF LPE SFDGDPASNTAPLPQLOLVFETLEITGYLYISAWPDSL 420  
QY 421 DLSVFQNLQVIRGRILHNGAYSLTLQGLISWGLRSLRELGSGLALIHNTLHLCFVHTV 480  
DB 421 DLSVFQNLQVIRGRILHNGAYSLTLQGLISWGLRSLRELGSGLALIHNTLHLCFVHTV 480  
QY 481 PWDQLFRNPHOALLHTANRPEDECEVGEGLACHOLCARGHCWGPGPTQCVCNCSQFLRGQEC 540  
DB 481 PWDQLFRNPHOALLHTANRPEDECEVGEGLACHOLCARGHCWGPGPTQCVCNCSQFLRGQEC 540  
QY 541 VEECRVLQGLPREYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKDPFPCVARC 600  
DB 541 VEECRVLQGLPREYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKDPFPCVARC 600  
QY 601 PSQVKPDLSPYMPKPPDEGACQPCPINCTHSCVDLDDKGCAPAEORASPLTS 653  
DB 601 PSQVKPDLSPYMPKPPDEGACQPCPINCTHSCVDLDDKGCAPAEORASPLTSIVSAVVG 660  
QY 654 654 653  
DB 661 ILLVVVLGVVFGILIKRQOKIRKYMRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720

Qy 654 ----- 653  
Db 721 RKVKVLGSGAGCTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGP 780  
Qy 654 ----- 653  
Db 781 YVSRLLGICLTSTVQLVTQMPYGCLLDHVRENRRGLSGODLLNWCMIKMGMSYLEDVR 840  
Qy 654 ----- 653  
Db 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGGKVPKMWALESIILRRFT 900  
Qy 654 ----- 653  
Db 901 HQSDVMSYGVTVWELMTFGAKPYDGIPIAREIPDLLEKGERLPQPICTIDVYIMVKKWM 960  
Qy 654 ----- QNEDLGASPLDSTFYRSLLDDDDMGDLVDA 684  
Db 961 IDSECRPRFRELVSFERNARDPQRFVVTQNEEDLGASPLDSTFYRSLLDDDDMGDLVDA 1020  
Qy 685 EYLVPPQGGFFCPCDPAGAGGMVHHRH 712  
Db 1021 EYLVPPQGGFFCPCDPAGAGGMVHHRH 1048

Search completed: December 5, 2003, 14:33:25  
Job time : 46.3599 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 5, 2003, 14:26:38 ; Search time 45.6401 Seconds  
(without alignments)  
3196.087 Million cell updates/sec

Title: US-09-854-356-6

Perfect score: 5078

Sequence: 1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 919

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.\*
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- 24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5078	100.0	919	21	Human HER-2/neu fu
2	5078	100.0	919	23	Her-2/neu extracel
3	4900	96.5	1255	17	HER-2/neu protein.
4	4900	96.5	1255	20	Human HER-2/neu on
5	4900	96.5	1255	21	Human HER-2/neu pr
6	4900	96.5	1255	21	Amino acid sequenc
7	4900	96.5	1255	22	Human HER-2/neu pr
8	4900	96.5	1255	22	Human HER-2/neu aci
9	4900	96.5	1255	23	Human Her-2 protei

10	4900	96.5	1255	23	AAE20479	Human Her-2/neu pr
11	4900	96.5	1255	23	AAE51143	Human Her-2/neu po
12	4900	96.5	1255	23	AAU77114	Human heregulin 2
13	4892	96.3	1255	21	AAU92620	Human tyrosine kin
14	4892	96.3	1255	22	AAE12130	HER2 transgene pla
15	4892	96.3	1255	22	AAE60167	Human HER-2 protei
16	4892	96.3	1255	23	AAE26349	Human HER2 antige
17	4892	96.3	1255	23	AAE26366	Human HER2 (ErBB2)
18	4892	96.3	1255	23	AAU74545	Breast cancer asso
19	4892	96.3	1255	24	ABR47447	Human Her-2/neu pr
20	4892	96.3	1255	24	ABP74708	Sequence of c-erbB
21	4857	95.6	1433	14	AAE39568	Human breast cance
22	4722	93.0	1223	23	AAU98923	Human HER-2/neu pr
23	4583	90.3	1200	21	AAE21208	Mouse Her-2/neu ex
24	4309.5	84.9	920	23	AAE51152	Mouse Her-2/neu ex
25	4309.5	84.9	926	23	AAE51153	Rat Her-2/neu prot
26	4138.5	81.5	1256	21	AAE21199	Rat Her-2/neu onco
27	4138.5	81.5	1256	23	AAE51144	Mouse Her-2/neu pr
28	4125.5	81.2	1256	21	AAE21206	Amino acid sequenc
29	4125.5	81.2	1256	23	AAE51151	Mouse Her-2/neu on
30	4125.5	81.2	1256	23	AAE51151	Human HER-2/neu fu
31	3954	77.9	712	21	AAE21204	Her-2/neu extracel
32	3954	77.9	712	23	AAE51149	Her-2-GM-CSF immuno
33	3632	71.5	782	18	AAE19764	Extracellular HER-
34	3628	71.4	653	21	AAE21200	Human Her-2/neu on
35	3628	71.4	653	23	AAE51145	Human ErbB2 oncopr
36	3590	70.7	645	22	AAE60408	Human ErbB2 extrac
37	3590	70.7	645	23	AAE61593	Human HER2 recepto
38	3590	70.7	645	23	ABG70753	DC88cFv-erbB2EC fu
39	3525	69.4	951	21	AAE44993	Extracellular port
40	3422	67.4	624	11	AAE08222	Rat Her-2/neu prot
41	3110.5	61.3	654	21	AAE21205	Rat Her-2/neu onco
42	3110.5	61.3	654	23	AAE51150	Human HER500 fusio
43	2585	50.9	564	22	AAE13110	Human HER500-rGM-C
44	2585	50.9	564	22	AAE13111	Human HER500 fusio
45	2573.5	50.7	555	22	AAE13108	

## ALIGNMENTS

RESULT 1	
AAE21203	
ID	AAE21203 standard; protein; 919 AA.
XX	
AC	AAE21203;
XX	
DT	12-JAN-2001 (first entry)
XX	
DE	Human HER-2/neu fusion protein.
XX	
KW	Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
KW	breast cancer; prostate cancer; ovarian cancer; lung cancer;
XX	colon cancer; fusion protein.
OS	Homo sapiens.
OS	Synthetic.
PN	WO200044899-A1.
XX	
XX	PD 03-AUG-2000.
PF	28-JAN-2000; 2000WO-US02164.
XX	
PR	29-JAN-1999; 99US-0117976.
PA	(CORI-) CORIXA CORP.
PA	(SMIK) SMITHKLINE BEECHAM.
XX	
PI	Cheever MA, Gheysen D;
XX	
DR	WPI; 2000-505976/45.
XX	

PT HER-2/neu extracellular domain/phosphorylation domain fusion proteins  
PT useful for vaccinating against breast, ovarian, colon, lung and  
PT prostate cancers -  
XX Claim 2; Fig 12; 128pp; English.

CC The present sequence is a fusion protein comprising the extracellular  
CC domain and the phosphorylation domain of the human HER-2/neu protein.  
CC HER-2/neu is a member of the tyrosine kinase family of receptor-like  
CC glycoproteins and shows homology to the epidermal growth factor receptor  
CC (EGFR). It probably plays a part in cell growth and/or differentiation.  
CC The HER-2/neu gene is an oncogene. HER-2/neu fusion proteins may be used  
CC to treat or prevent cancer by eliciting or enhancing an immune response  
CC to the HER-2/neu protein. They may be used to treat malignancies such as  
CC breast, ovarian, colon, lung and prostate cancers, and may be used as an  
CC antigen to vaccinate against these neoplasias.

XX SQ Sequence 919 AA;  
Query Match 100.0%; Score 5078; DB 21; Length 919;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 919; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELAALCRWGLLLALLPPGAASQVCTGDMKRLPASPETHLDMLRHLVQGCQVQGNL 60  
DB 1 MELAALCRWGLLLALLPPGAASQVCTGDMKRLPASPETHLDMLRHLVQGCQVQGNL 60  
QY 61 ELTYLPTNASLSFLQDIQEVQGVLIHNVQVPLRIIVRGTOIFEDNALAVLDNG 120  
DB 61 ELTYLPTNASLSFLQDIQEVQGVLIHNVQVPLRIIVRGTOIFEDNALAVLDNG 120  
QY 121 DPLNNTPTVGTASPGGLRELRLSLTEILKGGVLIQNPQLCYQDTILWKDIFHKNNOLA 180  
DB 121 DPLNNTPTVGTASPGGLRELRLSLTEILKGGVLIQNPQLCYQDTILWKDIFHKNNOLA 180  
QY 181 LTLIDTNRACHPCSPCKGSRGWESSEDCQSLRTVCAGCARCKGPLEPTDCHEQC 240  
DB 181 LTLIDTNRACHPCSPCKGSRGWESSEDCQSLRTVCAGCARCKGPLEPTDCHEQC 240  
QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPGRYTFGASCVTAC 300  
DB 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPGRYTFGASCVTAC 300  
QY 301 YNLTSDVGSCTLVCPHNOEVTAEQGTORCEKSKPCARVCVGLGMEHLREVRVTSAN 360  
DB 301 YNLTSDVGSCTLVCPHNOEVTAEQGTORCEKSKPCARVCVGLGMEHLREVRVTSAN 360  
QY 361 IQEFAGCKKIFGSLAFSPESFDGDPASNTAPLQEQVFTLEETGYLYISAWPDSL 420  
DB 361 IQEFAGCKKIFGSLAFSPESFDGDPASNTAPLQEQVFTLEETGYLYISAWPDSL 420  
QY 421 DLSVFQNLQVIRGRIHNGAYSILTLQGLISWGLSLRELGLALIHNTLCPVHTV 480  
DB 421 DLSVFQNLQVIRGRIHNGAYSILTLQGLISWGLSLRELGLALIHNTLCPVHTV 480  
QY 481 PNDLFRNPHOALLHTANPEDSCVGEGLACHOLCARGHCWGPQTQVCNCSQFLRGQSC 540  
DB 481 PNDLFRNPHOALLHTANPEDSCVGEGLACHOLCARGHCWGPQTQVCNCSQFLRGQSC 540  
QY 541 VEECRVLQGLPREYVNRHCLPCHPECQPNQSGSVTCFGEADQCVACAHYKPPFCVAC 600  
DB 541 VEECRVLQGLPREYVNRHCLPCHPECQPNQSGSVTCFGEADQCVACAHYKPPFCVAC 600  
QY 601 PSQVKPDLVSYMPTWKFPDEGACQPCINCHTSCVDLDDKGPAPQASPLTSQNEDLGP 660  
DB 601 PSQVKPDLVSYMPTWKFPDEGACQPCINCHTSCVDLDDKGPAPQASPLTSQNEDLGP 660  
QY 661 ASPLDSTFVRSLEDDMDGLVDABEYLVPOQGFCCPDAPGAGGMVHRHSSSTRSG 720  
DB 661 ASPLDSTFVRSLEDDMDGLVDABEYLVPOQGFCCPDAPGAGGMVHRHSSSTRSG 720  
QY 721 GDLTLGLEPSEBEEAPRSLAPSEGAGSDVFDGLGMGAAGLQSLTFHTDPPSLQRYSEDP 780

DB 721 GDLTLGLEPSEBEEAPRSLAPSEGAGSDVFDGLGMGAAGLQSLTFHTDPPSLQRYSEDP 780  
QY 781 TVPLPSETDGVVAPLTCSPOPEYVNPQDVVRPQPPREGPLPAARPAAGATLRRPKTLSPG 840  
DB 781 TVPLPSETDGVVAPLTCSPOPEYVNPQDVVRPQPPREGPLPAARPAAGATLRRPKTLSPG 840  
QY 841 KNGVVKDVFAFGAVENPEYLTPOGGAAPQHPHPPAFSPAFDNLVYWDQDPPERGAPPST 900  
DB 841 KNGVVKDVFAFGAVENPEYLTPOGGAAPQHPHPPAFSPAFDNLVYWDQDPPERGAPPST 900  
QY 901 FKGTPTAENPEYLGLDVFPV 919  
DB 901 FKGTPTAENPEYLGLDVFPV 919

RESULT 2  
AAM51148  
ID AAM51148 standard; Protein; 919 AA.  
XX  
AC AAM51148;  
DT 17-JUN-2002 (first entry)  
XX  
DE Her-2/neu extracellular domain-phosphorylation domain fusion.  
XX  
KW Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;  
KW tyrosine kinase; receptor; c-erbB2; gene therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Domain 1..653  
FT /note= "extracellular domain"  
FT Domain 654..919  
FT /note= "phosphorylation domain"  
XX  
XX WO200212341-A2  
XX 14-FEB-2002.  
XX  
XX 03-AUG-2001; 2001WO-US24283.  
XX 03-AUG-2000; 2000US-0632507.  
XX (CORI-) CORIXA CORP.  
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
XX Cheever MA, Gheysen D;  
XX WPI; 2002-241743/29.  
XX  
PT Her-2/neu fusion protein for treating or preventing cancer by eliciting  
PT or enhancing an immune response to the protein, has Her-2/neu  
PT extracellular domain fused to Her-2/neu intracellular or  
PT phosphorylation domain  
XX  
PS Claim 2; Fig 12; 141pp; English.  
XX  
CC The present sequence is that of a fusion protein between the  
CC extracellular domain and phosphorylation domain of human Her-2/neu  
CC (see AAM51143), an oncogenic self-protein and target for anti-cancer  
CC vaccines. The fusion protein can be obtained by recombinant DNA  
CC methods. Her-2/neu overexpression correlates with a poor prognosis  
CC in breast and ovarian cancers. The invention provides Her-2/neu  
CC fusion proteins, nucleic acids encoding them, viral vectors, and  
CC vaccines comprising the fusion proteins or nucleic acid molecules.  
CC In preferred fusion proteins, the extracellular domain of a  
CC Her-2/neu protein is fused to a Her-2/neu intracellular domain or  
CC phosphorylation domain (or its DeltaPD fragment). An immune  
CC response to Her-2/neu protein is elicited or enhanced by  
CC administering the fusion protein in the form of a vaccine, or by  
CC transfecting cells of an animal ex vivo with a nucleic acid  
CC encoding the fusion protein, and delivering the transfected cells

CC to the animal. The fusion proteins, nucleic acids, and isolated  
 CC specific T-cells are useful for inhibiting the development of a  
 CC cancer, especially breast, ovarian, colon, lung or prostate cancer  
 CC in a patient. T cells that specifically react with a Her-2/neu  
 CC fusion protein can be used to remove tumour cells from a sample in  
 CC order to inhibit the development of cancer in a patient.  
 XX  
 SQ Sequence 919 AA;

Query Match 100.0%; Score 5078; DB 23; Length 919;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 919; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELALCRLGGLLALLPPGAASVQCTGDMKRLPASPETHDMLRHLYQCCVQVQGNL 60  
 DB 1 MELALCRLGGLLALLPPGAASVQCTGDMKRLPASPETHDMLRHLYQCCVQVQGNL 60

QY 61 ELTYLPTNASLSFLQDIEVQGVLIHNVQVPLQRLRIVRGTQLFEDNVALAVLNG 120  
 DB 61 ELTYLPTNASLSFLQDIEVQGVLIHNVQVPLQRLRIVRGTQLFEDNVALAVLNG 120

QY 121 DPLNNTPTVTGASPGGLRELQRLSLEILKGGVLIQRPOLCVQDTILWKDIFHKNQOLA 180  
 DB 121 DPLNNTPTVTGASPGGLRELQRLSLEILKGGVLIQRPOLCVQDTILWKDIFHKNQOLA 180

QY 181 LTLIDTNRSRACHPCSPMKSGRCWGESSEDCQSLTRTVACGCCARCKGPLEPTDCHEQC 240  
 DB 181 LTLIDTNRSRACHPCSPMKSGRCWGESSEDCQSLTRTVACGCCARCKGPLEPTDCHEQC 240

QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTPESMPNPEGRYTFGASCVTACP 300  
 DB 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTPESMPNPEGRYTFGASCVTACP 300

QY 301 YNLSLTDVGSCTLVCPHNOVTADGTQRCCKPCARVCYGLGMEHLREVRAVTSAN 360  
 DB 301 YNLSLTDVGSCTLVCPHNOVTADGTQRCCKPCARVCYGLGMEHLREVRAVTSAN 360

QY 361 IQEFAGCKKIFGSLAFPLPSFGDPSANTAPQLQOVFETLEITGYLYISAWPDSLP 420  
 DB 361 IQEFAGCKKIFGSLAFPLPSFGDPSANTAPQLQOVFETLEITGYLYISAWPDSLP 420

QY 421 DLSVFQNLQVIRILHNGAYSILTQGLGISWGLRSLRELGLALIHNTLHCFVHTV 480  
 DB 421 DLSVFQNLQVIRILHNGAYSILTQGLGISWGLRSLRELGLALIHNTLHCFVHTV 480

QY 481 PWDQLFRNPHOALLHTANRPEDECVGEGGLACHQLCARGHCWGPPTQVCNCSQFLRGQEC 540  
 DB 481 PWDQLFRNPHOALLHTANRPEDECVGEGGLACHQLCARGHCWGPPTQVCNCSQFLRGQEC 540

QY 541 VEECRVLQGLPREYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKDPFPCVAC 600  
 DB 541 VEECRVLQGLPREYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKDPFPCVAC 600

QY 601 PSQVFPDLSYMPIKFPDEBEGACQPCINCTHSCVDLDDKGPAPQASPLTSQNEIDLGP 660  
 DB 601 PSQVFPDLSYMPIKFPDEBEGACQPCINCTHSCVDLDDKGPAPQASPLTSQNEIDLGP 660

QY 661 ASPLDSTFVRSLEDDMDGLVDABEYLVPQGFPCPDPAAGGVVHRRSSSTRSGG 720  
 DB 661 ASPLDSTFVRSLEDDMDGLVDABEYLVPQGFPCPDPAAGGVVHRRSSSTRSGG 720

QY 721 GDLTGLPSEBEPASPLAPSEBEGAGSDVFDGLGMAAGLQSLPDPSPLOQVSEDP 780  
 DB 721 GDLTGLPSEBEPASPLAPSEBEGAGSDVFDGLGMAAGLQSLPDPSPLOQVSEDP 780

QY 781 TVPLFSETDGYVAPLTCSQPEYVNPQDVRPQPPREGPLPAAPAGATLERPKTSLSP 840  
 DB 781 TVPLFSETDGYVAPLTCSQPEYVNPQDVRPQPPREGPLPAAPAGATLERPKTSLSP 840

QY 841 KNGVVKDVPFAGGAVENPBYLTQGGAAAPQHPHPPAFSPAFNLVYWDQDPERGAPPST 900  
 DB 841 KNGVVKDVPFAGGAVENPBYLTQGGAAAPQHPHPPAFSPAFNLVYWDQDPERGAPPST 900

QY 901 PKGPTAENPEYVLGLDVPV 919  
 DB 901 PKGPTAENPEYVLGLDVPV 919

RESULT 3  
 ID AAW01111 standard; Protein; 1255 AA.  
 XX AAW01111;  
 XX 01-JAN-1997 (first entry)  
 XX HER-2/neu protein.  
 XX HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase;  
 KW breast cancer; ovary cancer; colon cancer; lung cancer;  
 KW prostate cancer; immunisation; tumour; vaccine; vector.  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT 676..1255  
 FT Domain /label= Intracellular\_domain  
 FT /note= "claimed domain, useful for immunisation"  
 XX  
 XX W09630514-A1.  
 PD 03-OCT-1996.  
 XX  
 XX 28-MAR-1996; 96WO-US01689.  
 XX 31-MAR-1995; 95US-0414417.  
 XX (UNITW) UNIV WASHINGTON.  
 XX Cheever MA, Disis ML;  
 XX WPI; 1996-455361/45.  
 XX N-PSDB; AAT40739.  
 XX  
 XX DNA encoding HER-2-neu poly:peptide(s) - used for prevention or  
 XX treatment of malignancies with which the HER-2/neu oncogene is  
 XX associated  
 XX Claim 2; Page 56-61; 71pp; English.  
 XX  
 XX Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is  
 XX the product of the HER-2/neu oncogene (see also AAT40739). The  
 XX protein is over-expressed in various cancers, including breast,  
 XX ovarian, colon, lung and prostate. The intracellular domain of the  
 XX protein can be used to immunise an animal against a malignancy with  
 XX which the oncogene is associated. The polypeptide can be produced  
 XX in transformed host cells for use in immunisation. Alternatively,  
 XX animal cells are transfected in vivo or ex vivo with a viral vector  
 XX that directs expression of the polypeptide.

Query Match 96.5%; Score 4900; DB 17; Length 1255;  
 Best Local Similarity 73.2%; Pred. No. 0;  
 Matches 919; Conservative 0; Mismatches 0; Indels 336; Gaps 1;

QY 1 MELALCRLGGLLALLPPGAASVQCTGDMKRLPASPETHDMLRHLYQCCVQVQGNL 60  
 DB 1 MELALCRLGGLLALLPPGAASVQCTGDMKRLPASPETHDMLRHLYQCCVQVQGNL 60

QY 61 ELTYLPTNASLSFLQDIEVQGVLIHNVQVPLQRLRIVRGTQLFEDNVALAVLNG 120  
 DB 61 ELTYLPTNASLSFLQDIEVQGVLIHNVQVPLQRLRIVRGTQLFEDNVALAVLNG 120

QY 121 DPLNNTPTVTGASPGGLRELQRLSLEILKGGVLIQRPOLCVQDTILWKDIFHKNQOLA 180  
 DB 121 DPLNNTPTVTGASPGGLRELQRLSLEILKGGVLIQRPOLCVQDTILWKDIFHKNQOLA 180

Db 121 DPLNNTTPTVGTGASPGGLRELQSLTEILKGGVLIQRNPOLCYQDTILWKDIFHKNQLA 180  
QY 181 LTLIDNRSRACHPCSPMKSGSCWGESSEDCSLTRTVCAAGCARCKGPLPTDCCHEQC 240  
Db 181 LTLIDNRSRACHPCSPMKSGSCWGESSEDCSLTRTVCAAGCARCKGPLPTDCCHEQC 240  
QY 241 AAGCTGPKSDCLACILHFNHSGICELHCPALVYNTDTFESMPNPEGRYTFGASCVTACP 300  
Db 241 AAGCTGPKSDCLACILHFNHSGICELHCPALVYNTDTFESMPNPEGRYTFGASCVTACP 300  
QY 301 YNYLSTDVSGCTVLCPLHNOEVTABDGTQRCCKSPCARVCYGLGMEHLREVRATVSAN 360  
Db 301 YNYLSTDVSGCTVLCPLHNOEVTABDGTQRCCKSPCARVCYGLGMEHLREVRATVSAN 360  
QY 361 IQBFAGCKITFGSLAFIPESFEDGDPASNTAPLOPEQLQVFETLEEITGYLYISAWPDSL 420  
Db 361 IQBFAGCKITFGSLAFIPESFEDGDPASNTAPLOPEQLQVFETLEEITGYLYISAWPDSL 420  
QY 421 DLSVFQNLQVIRGRIILHNGAYSLTLOGLGTSWGLSLRELGLALIHNTHLCFVHTV 480  
Db 421 DLSVFQNLQVIRGRIILHNGAYSLTLOGLGTSWGLSLRELGLALIHNTHLCFVHTV 480  
QY 481 PWDQLFRNPHQALLHTANRPEDSCVGEGLACHOLCARGHCWGPGTQCVCNCSQFLRGQEC 540  
Db 481 PWDQLFRNPHQALLHTANRPEDSCVGEGLACHOLCARGHCWGPGTQCVCNCSQFLRGQEC 540  
QY 541 VEECRVLQGLPREYVNAHCLPCHPCOPONGSVTCFGEADOCVACAHYKOPPCVAVRC 600  
Db 541 VEECRVLQGLPREYVNAHCLPCHPCOPONGSVTCFGEADOCVACAHYKOPPCVAVRC 600  
QY 601 PSQVKPDLSTMPYIKFPEDEGACQPCPINCTHSCVDLDDKGCFAEQASPLTS----- 653  
Db 601 PSQVKPDLSTMPYIKFPEDEGACQPCPINCTHSCVDLDDKGCFAEQASPLTSIIISAVVG 660  
QY 654 ----- 653  
Db 661 ILLVVLGVVFGILIKRQOKIRKYTMRLLOTELVEPLTPSGAMPNOAQMRLKETEL 720  
QY 654 ----- 653  
Db 721 RKVKVLGSAFGTVYGIWIPDGENVKIPVAIKVLRENTSPKANKILDEAYVMAGVGP 780  
QY 654 ----- 653  
Db 781 YVSRLLGICLTSTVQLVTQMLPYGCLLDHVRENRGLSGDILLNWCMIAGKMSYLEDYR 840  
QY 654 ----- 653  
Db 841 LVHRDLAARNVLKSPNHVKITDFGLARLLIDETEYHADGGKVPKIMMALESILRRFT 900  
QY 654 ----- 653  
Db 901 HQSDVMSYGVTVWELMTFGAKPYDGPAREIPDLLEKGERLPQPPCTIDVYIMVWKVM 960  
QY 654 -----QNEDLGPASPLDSTFYRSILLEDDMDGLVDA 684  
Db 961 IDSECRPRELVSERWARDPQRFVQNEDLGPASPLDSTFYRSILLEDDMDGLVDA 1020  
QY 685 EYLVLPQOQFFCPDPAAGAGMHHRRSSSTRSGGDLTLGLEPSEEBAPRSPAPSG 744  
Db 1021 EYLVLPQOQFFCPDPAAGAGMHHRRSSSTRSGGDLTLGLEPSEEBAPRSPAPSG 1080  
QY 745 AGSDVFDGLGMAAGLQSLTHDPSPLQRYSEDPVLPSTDCGVAPLTCSPQPEV 804  
Db 1081 AGSDVFDGLGMAAGLQSLTHDPSPLQRYSEDPVLPSTDCGVAPLTCSPQPEV 1140  
QY 805 NQPDVRPQPPSPREGPLPAARAGATLERPKTLSPCKNGVWVDVAFGGAIVENPEYLTQ 864  
Db 1141 NQPDVRPQPPSPREGPLPAARAGATLERPKTLSPCKNGVWVDVAFGGAIVENPEYLTQ 1200  
QY 865 GGAAPQHPHPPAPSPADNLYWDQDPPPERGAPPSTFKGTPTAENPEYLGLDV 919  
Db 1201 GGAAPQHPHPPAPSPADNLYWDQDPPPERGAPPSTFKGTPTAENPEYLGLDV 1255

## RESULT 4

AAW92406  
ID AAW92406 standard; Protein; 1255 AA.

XX  
AC AAW92406;

XX  
DT 21-APR-1999 (first entry)

XX  
DE Human HER-2/neu oncogene protein.

XX  
KW HER-2/neu; oncogene; immune response; T cell; B cell; immunisation;

XX  
OS Homo sapiens.

XX  
FH Key Location/Qualifiers

XX  
FT Region 676..1255

XX  
PN US9869445-A.

XX  
PD 09-FEB-1999.

XX  
PF 01-APR-1996; 96US-0625101.

XX  
PR 01-APR-1996; 96US-0625101.

XX  
PR 17-MAR-1993; 93US-0033644.

XX  
PR 12-AUG-1993; 93US-0106112.

XX  
PR 31-MAR-1995; 95US-0414417.

XX  
PA (UNIW ) UNIV WASHINGTON.

XX  
PI Cheever MA, Disis ML;

XX  
DR WPI; 1999-152835/13.

XX  
DR N-PSDB; AAX01912.

XX  
PT Use of HER-2/neu polypeptides - for eliciting an immune response to

XX  
PT an HER-2/neu associated malignancy, particularly for treating or

XX  
XX preventing tumours

XX  
PS Claim 3; Column 31-38; 26pp; English.

XX  
CC This sequence represents the human HER-2/neu oncogene protein. A fragment

XX  
CC of this protein is used in a method for eliciting or enhancing an immune

XX  
CC response to HER-2/neu protein. The polypeptide can stimulate T cells and

XX  
CC B cells to produce an immune response to the HER-2/neu protein. The

XX  
CC method can be used for immunisation against a malignancy in which the

XX  
CC HER-2/neu oncogene is associated and in the treatment of an existing

XX  
CC tumour, or to prevent tumour occurrence or reoccurrence.

XX  
SQ Sequence 1255 AA;

Query Match 96.5%; Score 4900; DB 20; Length 1255;

Best Local Similarity 73.2%; Pred No. 0;

Matches 919; Conservative 0; Mismatches 0; Indels 336; Gaps 1;

QY 1 MELAALCRWGLLLALLPFGAASTQVCTGDMKRLPASPETHLDMRLHYQSCVVQGNL 60

Db 1 MELAALCRWGLLLALLPFGAASTQVCTGDMKRLPASPETHLDMRLHYQSCVVQGNL 60

QY 61 ELYLPTNASLSFLQDIOEVQGVLIQAHNOVQVPLQRLIRVRGTQFEDNYALVDNG 120

Db 61 ELYLPTNASLSFLQDIOEVQGVLIQAHNOVQVPLQRLIRVRGTQFEDNYALVDNG 120

QY 121 DPLNNTTPTVGTGASPGGLRELQSLTEILKGGVLIQRNPOLCYQDTILWKDIFHKNQLA 180

Db 121 DPLNNTTPTVGTGASPGGLRELQSLTEILKGGVLIQRNPOLCYQDTILWKDIFHKNQLA 180

QY 181 LTLIDNRSRACHPCSPMKSGSCWGESSEDCSLTRTVCAAGCARCKGPLPTDCCHEQC 240

Db 181 LTLIDNRSRACHPCSPMKSGSCWGESSEDCSLTRTVCAAGCARCKGPLPTDCCHEQC 240

Db 181 LTLIDTNRACRCHPCSPMCKGSRGWESSEDCQSLTRTVCAAGCARCKGPLPTDCCHQC 240  
Qy 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300  
Db 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300  
Qy 301 YNYLSTDVSGCTLVCPHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 360  
Db 301 YNYLSTDVSGCTLVCPHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 360  
Qy 361 IOEFAGCKIKFGLAFPLPSFDDPASNTAPLOPOLQVFTLEETGLYLSAMPDSL 420  
Db 361 IOEFAGCKIKFGLAFPLPSFDDPASNTAPLOPOLQVFTLEETGLYLSAMPDSL 420  
Qy 421 DLSVFQNLQVIRGRILHNGAYSILTQGLGSIWGLRSLRGLSLALHNTLHLCFVHTV 480  
Db 421 DLSVFQNLQVIRGRILHNGAYSILTQGLGSIWGLRSLRGLSLALHNTLHLCFVHTV 480  
Qy 481 PWDQLFRNPHQALLHTANRPEDECVEGLACHOLCARGHGWPGPTQCVNCSQFLRGQEC 540  
Db 481 PWDQLFRNPHQALLHTANRPEDECVEGLACHOLCARGHGWPGPTQCVNCSQFLRGQEC 540  
Qy 541 VEECRVLQGLPREYNARHCLCHBECOPONGSVTCFGEADQCVACAHYKDPPECVAC 600  
Db 541 VEECRVLQGLPREYNARHCLCHBECOPONGSVTCFGEADQCVACAHYKDPPECVAC 600  
Qy 601 PSGVKPDLSPYMKFPPDEBEGACQPCINCHSCVDLDDKGCPCARASPLTS 653  
Db 601 PSGVKPDLSPYMKFPPDEBEGACQPCINCHSCVDLDDKGCPCARASPLTS 653  
Qy 654 ----- 653  
Db 661 ILLVVVLGVFGILIKRQKIRKTYMRLLQETELVEPLTPSGAMPNQAMRILKTEL 720  
Qy 654 ----- 653  
Db 721 RKVKVLGSAFTVYKGIWIPGENVKIPVAIKVIRENTSPKANKEILDEAYVMAGVSP 780  
Qy 654 ----- 653  
Db 781 YVSRLLGICLTSTVQLVTLQMPYGCGLLDHVRNREGRGLSGQDLNWCMIAGKMSVLEDR 840  
Qy 654 ----- 653  
Db 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGKVPKIMWALESILRRFT 900  
Qy 654 ----- 653  
Db 901 HOSDVMSYGVTVWELMTFGAKPYDGIPIAREIPDLLEKGERLPQPPICTIDVYIMVKCM 960  
Qy 654 ----- 653  
Db 961 IDSECRPRELVSFRSARMARDPQFVVIQNEIDLPASPLDSTFVRSLEDDMGDLVDA 1020  
Qy 685 EYLVPOQGFPCDPAPGAGGMVHRHSSSTRSGGDLTLGLEPSEEAAPRSLAPSEG 744  
Db 1021 EYLVPOQGFPCDPAPGAGGMVHRHSSSTRSGGDLTLGLEPSEEAAPRSLAPSEG 1080  
Qy 745 AGSDVFDGDLGAAKGLQSLPHTDPSPLORYSEDTVPLPSETDGYVAPLTCSPQPIV 804  
Db 1081 AGSDVFDGDLGAAKGLQSLPHTDPSPLORYSEDTVPLPSETDGYVAPLTCSPQPIV 1140  
Qy 805 NOPDVRPQPPSPREGPLPAARPAAGATLERPKTSLPGKNGVKVDVAFGGAVENTPEYLPQ 864  
Db 1141 NOPDVRPQPPSPREGPLPAARPAAGATLERPKTSLPGKNGVKVDVAFGGAVENTPEYLPQ 1200  
Qy 865 GGAAPQPPHPPAFSPAFNLVYWDQDPPERGAPPSTFKGTAEENPEYLGDLVPV 919  
Db 1201 GGAAPQPPHPPAFSPAFNLVYWDQDPPERGAPPSTFKGTAEENPEYLGDLVPV 1255

RESULT 5  
AAB21198

ID AAB21198 standard; protein; 1255 AA.  
XX  
AC AAB21198;  
XX  
DT 12-JAN-2001 (first entry)  
XX  
DE Human HER-2/neu protein.  
XX  
KW Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;  
KW breast cancer; prostate cancer; ovarian cancer; lung cancer;  
KW colon cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200044899-A1.  
XX  
PD 03-AUG-2000.  
XX  
PF 28-JAN-2000; 2000WO-US02164.  
XX  
PR 29-JAN-1999; 99US-0117976.  
XX  
PA (CORI-) CORIXA CORP.  
PA (SMIK) SMITHKLINE BEECHAM.  
XX  
PI Cheever MA, Gheysen D;  
XX  
DR WPI; 2000-505976/45.  
DR N-PSDB; AAA89736.  
XX  
PT HER-2/neu extracellular domain/phosphorylation domain fusion proteins  
PT useful for vaccinating against breast, ovarian, colon, lung and  
PT prostate cancers -  
XX  
PS Claim 52; Fig 7; 128pp; English.  
XX

The present sequence is the human HER-2/neu protein. It is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-2/neu protein. It may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against these neoplasias.

SQ Sequence 1255 AA;

Query Match 96.5%; Score 4900; DB 21; Length 1255;  
Best Local Similarity 73.2%; Pred. No. 0;  
Matches 919; Conservative 0; Mismatches 0; Indels 336; Gaps 1;

Qy 1 MELAALCRWGLLLALLPPGAASCTVCTGDMKRLPASPETHLDMRLHLYQGCVVQGNL 60  
Db 1 MELAALCRWGLLLALLPPGAASCTVCTGDMKRLPASPETHLDMRLHLYQGCVVQGNL 60  
Qy 61 ELTYLPTNASLFLQDIOEVQGVYLIHNNQVQVPLQRLRIVRGTLQFEDNYALVDNG 120  
Db 61 ELTYLPTNASLFLQDIOEVQGVYLIHNNQVQVPLQRLRIVRGTLQFEDNYALVDNG 120  
Qy 121 DPLNNTTPVTGASPGGLRELQRLSLTELKGGVLIQRNPOLCYQDTILWKDI FHKNNQLA 180  
Db 121 DPLNNTTPVTGASPGGLRELQRLSLTELKGGVLIQRNPOLCYQDTILWKDI FHKNNQLA 180  
Qy 181 LTLIDTNRSRACHPCSPMCKGSRGWESSEDCQSLTRTVCAAGCARCKGPLPTDCCHQC 240  
Db 181 LTLIDTNRSRACHPCSPMCKGSRGWESSEDCQSLTRTVCAAGCARCKGPLPTDCCHQC 240  
Qy 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300  
Db 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

```
QY 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSAN 360
DB 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSAN 360
QY 361 IQEFAGCKKIFGSLAPLPSFPGDPAASNTAPLQPEOLQVFETLEIITGYLYISAWPDSL 420
DB 361 IQEFAGCKKIFGSLAPLPSFPGDPAASNTAPLQPEOLQVFETLEIITGYLYISAWPDSL 420
QY 421 DLSVFONQVIRGRILHNGAYSITLQGLGSLWGLRSLRELGLALIHNTLHLCFVHTV 480
DB 421 DLSVFONQVIRGRILHNGAYSITLQGLGSLWGLRSLRELGLALIHNTLHLCFVHTV 480
QY 481 PWDOLFRNPHOALLHTANPEDECVEGLACHQLCARGHCWPGPTQCVNCSQFLRGQEC 540
DB 481 PWDOLFRNPHOALLHTANPEDECVEGLACHQLCARGHCWPGPTQCVNCSQFLRGQEC 540
QY 541 VEECRVLOGLPREYVNAHCLPCHPECQPNQSVTCFGEADQCVACAHYKDPFPCVARC 600
DB 541 VEECRVLOGLPREYVNAHCLPCHPECQPNQSVTCFGEADQCVACAHYKDPFPCVARC 600
QY 601 PSGVKPDLSPYMPIWKPEDEGACQPCINCTHSCVDLDDKGCPCAEORASPLTS----- 653
DB 601 PSGVKPDLSPYMPIWKPEDEGACQPCINCTHSCVDLDDKGCPCAEORASPLTSIIISAVVG 660
QY 654 ----- 653
DB 661 ILLVVVLGVVFGILLIKRQOKIRKYTMRLLOETELVEPLTPSGAMPNQAQMRILKETEL 720
QY 654 ----- 653
DB 721 RKVKVLGSGAFGVYKGIWIPDGENVKIPVAKVIRENTSPRANKIILDEAYVMAGVGP 780
QY 654 ----- 653
DB 781 YVSRLLGICLTSTVQLVTQLMPYGCILLDHVRENRGLSQDLNWCQMIAKMSYLEVDR 840
QY 654 ----- 653
DB 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDDTEYHADGGKVPKKNWALSILERRFT 900
QY 654 ----- 653
DB 901 HQSDVMSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTTIDVYIMVKWM 960
QY 654 -----ONEDLGPASPLDSTFYRSILLEDDMDGLVDA 684-
DB 961 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEIDLGPASPLDSTFYRSILLEDDMDGLVDA 1020
QY 685 EYLVVPOQGFCCPDPAAGAGMVHRRSSSTRSGGDLTLGLPSEEEAPRSPAPSEG 744
DB 1021 EYLVVPOQGFCCPDPAAGAGMVHRRSSSTRSGGDLTLGLPSEEEAPRSPAPSEG 1080
QY 745 AGSDVFDGLGMAAGKLSLTHDPSPLQRYSEDTVPPLPSETDGYVAPLTCSPQPEYV 804
DB 1081 AGSDVFDGLGMAAGKLSLTHDPSPLQRYSEDTVPPLPSETDGYVAPLTCSPQPEYV 1140
QY 805 NQPDVFPQPPSPREGPLPAARPAAGATLERPKTLSPGKNGVWKDVAFAGAVENPEYLTQ 864
DB 1141 NQPDVFPQPPSPREGPLPAARPAAGATLERPKTLSPGKNGVWKDVAFAGAVENPEYLTQ 1200
QY 865 GGAAPQHPHPPAFSPADNLYWDDQPPBERGAPPSTFKGTPTAENPEYLGLOVPV 919
DB 1201 GGAAPQHPHPPAFSPADNLYWDDQPPBERGAPPSTFKGTPTAENPEYLGLOVPV 1255
```

RESULT 6

AAY84780

ID AAY84780 standard; Protein; 1255 AA.

XX

AC AAY84780;

XX

DT 08-AUG-2000 (first entry)

```
XX Amino acid sequence of the SPLICE erbB-2 receptor protein.
DE SPLICE erbB-2 receptor protein; cell transformation disorder; cancer;
XX tumor cell proliferation; tissue degeneration; arthropathy;
KW bone resorption; inflammatory disease; degenerative disorder;
KW wound healing.
XX Homo sapiens.
OS WO200020579-A1.
PN 13-APR-2000.
PD 01-OCT-1999; 99WO-CA00912.
XX 02-OCT-1998; 98US-0165192.
XX (UYMC-) UNIV MCMASTER.
PI Muller WJ, Siegel PW;
XX WPI; 2000-303768/26.
DR N-PSDB; AAA14812.
XX Nucleic acid encoding an erbB 2 receptor protein designated SPLICE
PT erbB-2, inhibitors of the protein are useful for treatment of cancer
PS Claim 3; Fig 2; 60pp; English.
XX The present sequence represents a SPLICE erbB-2 receptor protein. The
CC protein has an in-frame deletion of 16 amino acids, 2 of which are
CC conserved cysteine residues, compared to the unspliced protein. The
CC erbB-2 polynucleotide is used to construct probes for detecting
CC disorders of cell transformation such as cancer. Antibodies to the
CC protein may be used to detect SPLICE erbB-2 in a sample. Agents
CC (e.g. antisense oligonucleotides) which inhibit the expression of
CC SPLICE erbB-2 are useful for reducing tumor cell proliferation and
CC treating cancer. Substances which stimulate SPLICE erbB-2 are useful
CC for treating conditions involving damaged cells including conditions
CC in which degeneration of tissue occurs, such as arthropathy, bone
CC resorption, inflammatory diseases, degenerative disorders of the
CC central nervous system and wound healing.
XX Sequence 1255 AA;
```

```
Query Match 96.5%; Score 4900; DB 21; Length 1255;
Best Local Similarity 73.2%; Pred. No. 0;
Matches 919; Conservative 0; Mismatches 0; Indels 336; Gaps 1;
QY 1 MELAALCRWGLLLALLPPGAASQVCTGDMKRLPASPETHLDMRLHYQCGVVOGNL 60
DB 1 MELAALCRWGLLLALLPPGAASQVCTGDMKRLPASPETHLDMRLHYQCGVVOGNL 60
QY 61 ELTYLPTNASLSFLQDIOEVQGYVLIHQNVRQVPLQRLRIVRGTLPEDNYALAVLDNG 120
DB 61 ELTYLPTNASLSFLQDIOEVQGYVLIHQNVRQVPLQRLRIVRGTLPEDNYALAVLDNG 120
QY 121 DPLNNTTPTVGTASPGGLRELQRLRSITLKGVLQRLNORPOLCYQDTILWKDIFHKNNQLA 180
DB 121 DPLNNTTPTVGTASPGGLRELQRLRSITLKGVLQRLNORPOLCYQDTILWKDIFHKNNQLA 180
QY 181 LTLIDTNRSRACHPCSPMKSGRCWGESSEDCQSILTRTVACGGCARCKGLPTDCCHEOC 240
DB 181 LTLIDTNRSRACHPCSPMKSGRCWGESSEDCQSILTRTVACGGCARCKGLPTDCCHEOC 240
QY 241 AAGCTGPKHSDCLACLFHFNHSGICELHCPALVYNTDTFESMPNPEGRYTFGASCVTACP 300
DB 241 AAGCTGPKHSDCLACLFHFNHSGICELHCPALVYNTDTFESMPNPEGRYTFGASCVTACP 300
QY 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSAN 360
DB 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSAN 360
```



```
QY 481 PWDQLFRNPHQALLHTANRPEDECVEGLACHQLCARGHCWGPGTQCVCNCSQFLRGQEC 540
Db 481 PWDQLFRNPHQALLHTANRPEDECVEGLACHQLCARGHCWGPGTQCVCNCSQFLRGQEC 540
QY 541 VBECRVLOGLPREYVYVNRARCLCHPECCQONGSVTCFGEADQCACAHYKDPPEFCVARC 600
Db 541 VBECRVLOGLPREYVYVNRARCLCHPECCQONGSVTCFGEADQCACAHYKDPPEFCVARC 600
QY 601 PSGVKPDLSPYMPKWKFPDEEGACQPCINCTHSCVDLDDKGCAPABORASPLTS----- 653
Db 601 PSGVKPDLSPYMPKWKFPDEEGACQPCINCTHSCVDLDDKGCAPABORASPLTSIISAVVG 660
QY 654 ----- 653
Db 661 ILLVVVLGVVGLIKRQKIRKVTMRLLQETELVEPLTPSGAMPNQAMRILKETEL 720
QY 654 ----- 653
Db 721 RKVKVLGSGAFGVYKGIWIPDENVKIPVAIKVLRNTPSKANKRKEILDEAYVMAGVSP 780
QY 654 ----- 653
Db 781 YVSRLLGICLTSTVQLVTQMPYGCLLDHVRENHRLGSGQDILLNMCWQIAKMSYLEVDVR 840
QY 654 ----- 653
Db 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGGKVPKIKWMALESILRRRT 900
QY 654 ----- 653
Db 901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPTCTIDVYMIWVKWM 960
QY 654 ----- 653
Db 961 IDSECRPRELVSEFSRWARDPQRFVITQNEDLGPASPLDSTFYRSLLEDDMDGLVDA 1020
QY 685 EYLVLPQOQFFCPDPAPGAGVHHRSSSTRSGGDLTLGLEPSEEEAPRSLAPSEG 744
Db 1021 EYLVLPQOQFFCPDPAPGAGVHHRSSSTRSGGDLTLGLEPSEEEAPRSLAPSEG 1080
QY 745 AGSDVPDGLGMAAGLQSLPHTDPSPLQRYSEDPVPLPSETDGYVAPLTCSPQPEYV 804
Db 1081 AGSDVPDGLGMAAGLQSLPHTDPSPLQRYSEDPVPLPSETDGYVAPLTCSPQPEYV 1140
QY 805 NOPDVRPQPPSPREGPLPAARPAAGATLERPKTLSPCKNGVVDVFAFGAVENPEYLTQ 864
Db 1141 NOPDVRPQPPSPREGPLPAARPAAGATLERPKTLSPCKNGVVDVFAFGAVENPEYLTQ 1200
QY 865 GGAAPQHPPPPAFSPAFDNLVYWDQPPPERGAPPSTFKGTPTAENPEYLGLDVVPV 919
Db 1201 GGAAPQHPPPPAFSPAFDNLVYWDQPPPERGAPPSTFKGTPTAENPEYLGLDVVPV 1255
```

## RESULT 8

AAG88267

ID AAG88267 standard; Protein; 1255 AA.

XX

AC AAG88267;

XX

DT 11-SEP-2001 (first entry)

XX

DE HER2/neu amino acid sequence.

XX

KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;

XX

KW Immune response; vaccine; tumour; cancer; cytotoxic; immunostimulant;

XX

KW Tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

XX

OS Homo sapiens.

XX

PN WO200141787-A1.

XX

PD 14-JUN-2001.

XX

```
PF 11-DEC-2000; 2000WO-US33591.
PR 10-DEC-1999; 99US-0458299.
XX (EPIM-) EPIMUNE INC.
PA Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
PI Keogh E;
XX MPI; 2001-374995/39.
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing
PT cellular immune responses for the prevention and treatment of cancer -
XX Disclosure; Page 15; 1999p; English.
XX The present invention describes isolated prepared HER2/neu epitopes (I).
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
CC culture in vitro and binds to a complex of an epitope (I), bound to a
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
CC and a second epitope and the peptide is less than 50 contiguous amino
CC acids that have 100% identity with a native peptide sequence of HER2/neu;
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising
CC (I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic
CC and immunostimulant activities, and can be used in vaccines. (I), (II)
CC and (III) are useful for inducing cellular immune responses for the
CC prevention and treatment of cancer. (I) and (II) are useful for
CC monitoring or evaluating an immune response to a tumour-associated
CC antigen when incubated with a T lymphocyte sample from a patient and
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope
CC based vaccines mean that immunosuppressive epitopes that may be present
CC in whole antigens may be avoided. Selected epitopes may be combined to
CC enhance immunogenicity. The possible pathological side effects caused by
CC infectious agents or whole protein antigen is eliminated. The vaccine
CC provides the ability to direct and focus an immune response to multiple
CC selected antigens from the same pathogen. Epitope-based anti-tumour
CC vaccines provides the opportunity to combine epitopes derived from
CC multiple tumour-associated molecules addressing the problem of tumour-
CC tumour variability and reducing the likelihood of tumour escape due to
CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in
CC the exemplification of the present invention.
XX Sequence 1255 AA;
```

Query Match 96.5%; Score 4900; DB 22; Length 1255;

Best Local Similarity 73.2%; Pred. No. 0;

Matches 919; Conservative 0; Mismatches 0; Indels 336; Gaps 1;

QY 1 MELAALCRWGLLALLPFGAASVQCTGDMKRLPASPETHLDMRLHYQGVVQGNL 60

Db 1 MELAALCRWGLLALLPFGAASVQCTGDMKRLPASPETHLDMRLHYQGVVQGNL 60

QY 61 ELTYLPTNASLFLQDIOEVQGVYLIANHVRQVPLQRLRIVRGTLFEDNVALAVLDNG 120

Db 61 ELTYLPTNASLFLQDIOEVQGVYLIANHVRQVPLQRLRIVRGTLFEDNVALAVLDNG 120

QY 121 DPLNNTTPVTGASPGGLRELQRLSLTEILKGVLIQRNPOLCYQDTILWKDIFHKQNQLA 180

Db 121 DPLNNTTPVTGASPGGLRELQRLSLTEILKGVLIQRNPOLCYQDTILWKDIFHKQNQLA 180

QY 181 LTLIDTNRSRACHPCSPMKSGRCWGESSEDCQSLTRTVACGGCARCKGPLPTDCCHEQC 240

Db 181 LTLIDTNRSRACHPCSPMKSGRCWGESSEDCQSLTRTVACGGCARCKGPLPTDCCHEQC 240

QY 241 AAGCTGPKHSDCLACLFHFNHSGICBLHPALVTYNTDFESPNPEGRYTFGASCVTACP 300

Db 241 AAGCTGPKHSDCLACLFHFNHSGICBLHPALVTYNTDFESPNPEGRYTFGASCVTACP 300

QY 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSPCARVCYGLGMEHLREVRVTSAN 360

Db 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSPCARVCYGLGMEHLREVRVTSAN 360



QY 481 PWDQFRNPHQALLHTANRPEDECVEGLACHQLCARGHCWGPGPTQCVCNCSQFLRGQEC 540  
DB 481 PWDQFRNPHQALLHTANRPEDECVEGLACHQLCARGHCWGPGPTQCVCNCSQFLRGQEC 540  
QY 541 VBECRVLQGLPREYNARHCLPCHBPCQPNQSGSVTCFGEADQCACAHYKDPKPPFCVARC 600  
DB 541 VBECRVLQGLPREYNARHCLPCHBPCQPNQSGSVTCFGEADQCACAHYKDPKPPFCVARC 600  
QY 601 PSQVKEDLSYMPITWKEPDEGACQPCINCTHSCVDLDDKGCFAORASPLTS----- 653  
DB 601 PSQVKEDLSYMPITWKEPDEGACQPCINCTHSCVDLDDKGCFAORASPLTSIIISAVVG 660  
QY 654 ----- 653  
DB 661 ILLVVVLGVVGLILKERQKIRKYTMRLLQETELVEPLTPSGAMPNQAMRILKETEL 720  
QY 654 ----- 653  
DB 721 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRNTPSKANKBEILDYAVMAGVGSF 780  
QY 654 ----- 653  
DB 781 YVSRLLGICLTSTVQLVLTQMPYVGLLDHVHNRGRGLSGQDLLNWCMTAKGMSYLEVDR 840  
QY 654 ----- 653  
DB 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGGKVPKIKWALBSILRRFT 900  
QY 654 ----- 653  
DB 901 HQSDVMSYGVTVWELMTFGAKPYDGIPIAREIPDLLEKGERLPQPPICITIDVYIMVVKWM 960  
QY 654 -----QNEDLGPASPLDSTFYRESLLEDDMDGLVDA 684  
DB 961 IDSECRPRFRELVSFERSMARDPQRFVITQNEDLGPASPLDSTFYRESLLEDDMDGLVDA 1020  
QY 685 EYLVVQOQFFCPDPAPGAGVHHRHRSSTRSGGDLTLGLEPSEEAAPSRLAPSG 744  
DB 1021 EYLVVQOQFFCPDPAPGAGVHHRHRSSTRSGGDLTLGLEPSEEAAPSRLAPSG 1080  
QY 745 AGSDVFDGLGMAAGLSPLTHDPSPLQRYSEDTVPLPSETDGYVAPLTCSPQPEYV 804  
DB 1081 AGSDVFDGLGMAAGLSPLTHDPSPLQRYSEDTVPLPSETDGYVAPLTCSPQPEYV 1140  
QY 805 NQPDVPEPPSPREGPLPAARPAATLERPKTLLSPGKNGVWVDVFAFGAVENPEYLTQ 864  
DB 1141 NQPDVPEPPSPREGPLPAARPAATLERPKTLLSPGKNGVWVDVFAFGAVENPEYLTQ 1200  
QY 865 GGAAPQHPPPAFSPAFDNLVYWDQPPPERGAPPSTFKGTPTAENPEYLGLDVVPV 919  
DB 1201 GGAAPQHPPPAFSPAFDNLVYWDQPPPERGAPPSTFKGTPTAENPEYLGLDVVPV 1255

RESULT 10  
AAE20479  
ID AAE20479 standard; Protein; 1255 AA.  
AC AAE20479;  
XX  
DT 01-JUL-2002 (first entry)  
XX  
DE Human Her-2/neu protein.  
XX  
KW Human; Her-2/Neu protein; immune response; gene therapy; breast cancer;  
KW human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 1021..1030  
FT /note= "Naturally processed HLA-B44-restricted epitope"  
XX

PN WO200214503-A2.  
XX  
PD 21-FEB-2002.  
XX  
PF 14-AUG-2001; 2001WO-US41733.  
XX  
PR 14-AUG-2000; 2000US-225152P.  
PR 28-SEP-2000; 2000US-236428P.  
XX 21-FEB-2001; 2001US-270520P.  
XX (CORI-) CORIXA CORP.  
PA  
XX Hand-zimmermann S, Cheever MA, Foy TM, Lodes MJ, Kalos MD;  
PI McNeill PD, Vedwick TS;  
XX  
XX WPI; 2002-280758/32.  
DR N-PSDB; AAD32743.  
XX  
PT Novel isolated Her-2/Neu polypeptide composition useful for therapy,  
PT prevention and diagnosis of cancer, preferably breast cancer -  
XX  
PS Disclosure; Page 114-117; 129pp; English.  
XX  
CC The invention relates to an isolated Her-2/Neu polypeptide composition  
CC effective for eliciting an immune response. The invention is useful for  
CC eliciting an immune response in a patient, where the patient is human  
CC leukocyte antigen (HLA)-B44 positive or is affected with breast cancer.  
CC The composition is useful for the therapy and diagnosis of cancer,  
CC preferably breast cancer, in pharmaceutical compositions, e.g., vaccine  
CC and other compositions for the diagnosis, prevention and treatment of  
CC human malignancies, for stimulating and/or expanding T cells specific for  
CC Her-2/Neu polypeptide and for inhibiting the development of cancer in a  
CC patient. The invention is useful for stimulating a T cell response in a  
CC human patient, as probe or primer for nucleic acid hybridisation, to  
CC selectively form duplex molecules with complementary stretches of the  
CC entire Her-2/Neu gene or gene fragments of interest, to isolate a full  
CC length gene from a suitable library, and to direct expression of a  
CC polypeptide in appropriate host cells. The composition is useful in  
CC prophylactic or therapeutic applications and for the treatment of cancer,  
CC preferably for the immunotherapy of breast cancer and other Her-2/Neu-  
CC associated malignancies. The invention is useful in gene therapy. The  
CC present sequence is human Her-2/neu protein.  
XX  
SQ Sequence 1255 AA;

Query Match 96.5%; Score 4900; DB 23; Length 1255;  
Best Local Similarity 73.2%; Pred No. 0;  
Matches 919; Conservative 0; Mismatches 0; Indels 336; Gaps 1;  
QY 1 MELAALCRWGLLLALLPFGAASQVCTGTMKRLRLPASPTHLDMLRHLVYQGCQVVOGNL 60  
DB 1 MELAALCRWGLLLALLPFGAASQVCTGTMKRLRLPASPTHLDMLRHLVYQGCQVVOGNL 60  
QY 61 ELTYLPTNASLFLQDIQEVQGVYLIHNVQVPLQRLRIVRGTLQFEDNVALAVLDNG 120  
DB 61 ELTYLPTNASLFLQDIQEVQGVYLIHNVQVPLQRLRIVRGTLQFEDNVALAVLDNG 120  
QY 121 DPLNNTTPTVGTASPGGLRELQRLSLTEILKGVLIQRPOLCYQDTILWKDIFHKNNOLA 180  
DB 121 DPLNNTTPTVGTASPGGLRELQRLSLTEILKGVLIQRPOLCYQDTILWKDIFHKNNOLA 180  
QY 181 LTLIDNTRSRACHPCSPMKGSRGWGSESDCQSLTRTVACGGCARCKPLPTDCCHEQC 240  
DB 181 LTLIDNTRSRACHPCSPMKGSRGWGSESDCQSLTRTVACGGCARCKPLPTDCCHEQC 240  
QY 241 AAGCTGPKHSDCLACILFHNHSGICELHCPALVTYNTDFESMPNPEGRYTFGASCYTAC 300  
DB 241 AAGCTGPKHSDCLACILFHNHSGICELHCPALVTYNTDFESMPNPEGRYTFGASCYTAC 300  
QY 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSPCARVCYGLGMEHLREVAVTSAN 360  
DB 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSPCARVCYGLGMEHLREVAVTSAN 360

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QY 361 IOEFAGCKKIFGSLAFLESFSGDPSANTAPLOPEQLQVFFETLEITGYLYISAWPDSLP 420
Db 361 IOEFAGCKKIFGSLAFLESFSGDPSANTAPLOPEQLQVFFETLEITGYLYISAWPDSLP 420
QY 421 DLSVFQNLQVIRGRILHNGAYSLTQGLGISWGLRLSRELGSGLALHNNTHLCFVHTV 480
Db 421 DLSVFQNLQVIRGRILHNGAYSLTQGLGISWGLRLSRELGSGLALHNNTHLCFVHTV 480
QY 481 PWDQLFRNPHQALLHTANRPEDECVEGEGACHOLCARGHCWGPPTQCVNCSQFLRGQEC 540
Db 481 PWDQLFRNPHQALLHTANRPEDECVEGEGACHOLCARGHCWGPPTQCVNCSQFLRGQEC 540
QY 541 VEECRVLOGLPREYNARHCLPCHPECOFQNGSVTCFGEADQCACAHYKDPDPPCVARC 600
Db 541 VEECRVLOGLPREYNARHCLPCHPECOFQNGSVTCFGEADQCACAHYKDPDPPCVARC 600
QY 601 PSQVKPDLSYMPIWKFPPDEEGACQPCINCHTSCVDLDDKGCFAORASPLTS 653
Db 601 PSQVKPDLSYMPIWKFPPDEEGACQPCINCHTSCVDLDDKGCFAORASPLTS 653
QY 654 ----- 653
Db 654 ----- 653
QY 721 RKVKVLGSGAGTVYKIWDGENVKIPVAIKVLENTSPKANKEILDEAYVMAGVSP 780
QY 654 ----- 653
Db 781 YVSRLLGICLTSTVLQTLMPYGLCLDVRNRCGLSGQDLLANCMQIAKMSYLEDVR 840
QY 654 ----- 653
Db 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGCKVPIKMALESILRRFT 900
QY 654 ----- 653
Db 901 HQSDVMSYGVTVWELMTFGAKPYDIPAREIPDLLEKGERLPQPPICTIDVYMIWVKWM 960
QY 654 ----- 653
Db 961 IDSECRPRFRELVSFSRWARDPQRFVVIQNEBGLFASPLDSTFYRSLLEDDDMGDLYDA 1020
QY 685 EBYLVPQGFCDPAPAGAGVHHRSSSTRSGGDLTLGLEPSEEAAPRSLAPSEG 744
Db 1021 EBYLVPQGFCDPAPAGAGVHHRSSSTRSGGDLTLGLEPSEEAAPRSLAPSEG 1080
QY 745 AGSDVFDGDLGMAAGLQSLPHTDPSPLQRYSEDTVPLPSETDGYVAPLTCSPQPEYV 804
Db 1081 AGSDVFDGDLGMAAGLQSLPHTDPSPLQRYSEDTVPLPSETDGYVAPLTCSPQPEYV 1140
QY 805 NOPDVRPQPPSPREGFLPAARPAAGATLBRPRTLSPGKNGVVKDVPAGGAVENPYLTPQ 864
Db 1141 NOPDVRPQPPSPREGFLPAARPAAGATLBRPRTLSPGKNGVVKDVPAGGAVENPYLTPQ 1200
QY 865 GGAAPQHPHPPAFSAFNLVYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 919
Db 1201 GGAAPQHPHPPAFSAFNLVYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
```

## RESULT 11

AA051143

ID AA051143 standard; Protein; 1255 AA.

XX AC AA051143;

XX DT 17-JUN-2002 (first entry)

DE Human Her-2/neu oncogene - encoded p185 glycoprotein.

KW Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;  
tyrosine kinase; receptor; c-erbB2; gene therapy.

```
XX Homo sapiens.
OS 1. 653
FH Key Location/Qualifiers
FT Domain /note= "extracellular domain"
FT Domain /note= "intracellular domain"
FT Domain /note= "phosphorylation domain"
XX WO2000212341-A2.
PN 14-FEB-2002.
PD 03-AUG-2001; 2001WO-US24283.
PF 03-AUG-2000; 2000US-0632507.
PR (CORI-) CORIXA CORP.
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA Cheever MA, Gheysen D;
XX WPI; 2002-241743/29.
XX N-PSDB; ABA92250.
DR Her-2/neu fusion protein for treating or preventing cancer by eliciting
or enhancing an immune response to the protein, has Her-2/neu
extracellular domain fused to Her-2/neu intracellular or
phosphorylation domain
XX Claim 68; Fig 7; 141pp; English.
```

The present sequence is that of human Her-2/neu (p185 glycoprotein or c-erbB2), an oncogenic self-protein and target for anti-cancer vaccines. The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins. It comprises an extracellular domain with homology to the epidermal growth factor receptor (EGFR), a highly hydrophobic transmembrane domain and a C-terminal intracellular domain that also shows homology to EGFR. Its overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu fusion proteins, nucleic acids encoding them, viral vectors, and vaccines comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain of a Her-2/neu protein is fused to a Her-2/neu intracellular domain or phosphorylation domain (or its DeltaPD fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal *ex vivo* with a nucleic acid encoding the fusion protein, and delivering the transfected cells to the animal. The fusion proteins, nucleic acids, and isolated specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in order to inhibit the development of cancer in a patient.

XX Sequence 1255 AA;

Query Match 96.5%; Score 4900; DB 23; Length 1255;  
Best Local Similarity 73.2%; Pred. No. 0;  
Matches 919; Conservative 0; Mismatches 0; Indels 336; Gaps 1;

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QY 1 MELAALCRWGLLLALLPPGAASVCTCTDKMLRPLASPETHDMLRLHYQCQVQGNL 60
Db 1 MELAALCRWGLLLALLPPGAASVCTCTDKMLRPLASPETHDMLRLHYQCQVQGNL 60
QY 61 ELTYLPTNASTLFLQDIOEQVGYLIIAHNQVRQVPLQRLIRVGTQLPEDNYALVLDNG 120
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Db 61 ELTYLPTNASLFLQDIOEVQGVLIHQNVRQVPLQRLRIRVGTQLFDNVALAVLDNG 120  
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Db 121 DPLNNTTPTVGTASPGGLRELQRLSLEILKGVLIQORNPCQYQDTILWKDIFHKNNQLA 180  
QY 181 LTLIDNRRACHPCSPMKGSRGWESSEDCQSLTRTVACGACRCKGPLPTDCCHQC 240  
Db 181 LTLIDNRRACHPCSPMKGSRGWESSEDCQSLTRTVACGACRCKGPLPTDCCHQC 240  
QY 241 AGCTGPKHSDCLACHFNHSGICELHCPALVTYNTDTEESMPNPEGRYTFGASCVTACP 300  
Db 241 AGCTGPKHSDCLACHFNHSGICELHCPALVTYNTDTEESMPNPEGRYTFGASCVTACP 300  
QY 301 YNVLSTDVGSCTLVCPHLNQEVTAEDGTORCEKSKPCARVCYGLGMEHLREVRAVTSAN 360  
Db 301 YNVLSTDVGSCTLVCPHLNQEVTAEDGTORCEKSKPCARVCYGLGMEHLREVRAVTSAN 360  
QY 361 IQEFAGCKKIFGSLAFPLPESFDGDPASNTAPLQPEQLQVFETLEETGYLYISAWPDSL 420  
Db 361 IQEFAGCKKIFGSLAFPLPESFDGDPASNTAPLQPEQLQVFETLEETGYLYISAWPDSL 420  
QY 421 DLSVFQNLQVIRGRILHNGAYSILTQGLGISWLGRLSRELGSGLALIHNTLHLCFVHTV 480  
Db 421 DLSVFQNLQVIRGRILHNGAYSILTQGLGISWLGRLSRELGSGLALIHNTLHLCFVHTV 480  
QY 481 PWDQLFRNPHQALLHTANRPEBCEVGEGLACHQLCARGHCWPGPTQCVCNCSQFIRGQBC 540  
Db 481 PWDQLFRNPHQALLHTANRPEBCEVGEGLACHQLCARGHCWPGPTQCVCNCSQFIRGQBC 540  
QY 541 VEECRVQLPREYVNAHCLCHPECPQNGSVTCFGEADQCACAHYKDPFPFCVARC 600  
Db 541 VEECRVQLPREYVNAHCLCHPECPQNGSVTCFGEADQCACAHYKDPFPFCVARC 600  
QY 601 PSGVKPDLSPYMPWKFPDEGACQPCINCTHSCVDLDDKGCPCAEORASPLTS----- 653  
Db 601 PSGVKPDLSPYMPWKFPDEGACQPCINCTHSCVDLDDKGCPCAEORASPLTSISAVVG 660  
QY 654 ----- 653  
Db 661 ILLVVVLGVVFGILIKRQOKIRKYMRLLOETELVEPLTPSGAMPNAQMRILKETEL 720  
QY 654 ----- 653  
Db 721 RKVKVLGSAFGTVYKGIWIPDGENVKIPVAIKVIRENTSPRANKBEILDEAYVMAGVSP 780  
QY 654 ----- 653  
Db 781 YVSRLLGICLTSTVQLVQLMPYGLLDHVRNRRGLSGQDLLNWCWQIAKGMYSLELYR 840  
QY 654 ----- 653  
Db 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGKVPKVMWLESILRRRT 900  
QY 654 ----- 653  
Db 901 HQSDVMSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPOPPICITIDVYIMVKCW 960  
QY 654 -----ONEDLGPASPLDSTFYRSLLDDDDMGDLVDA 684  
Db 961 IDSECRPRFRELVSERFARMARDPQREVVQNEEDLGPASPLDSTFYRSLLDDDDMGDLVDA 1020  
QY 685 EBYLVQOQFFCDDPAPAGGWHHRSSSTRSGGDLTLGLEPSEEAAPSPAPSE 744  
Db 1021 EBYLVQOQFFCDDPAPAGGWHHRSSSTRSGGDLTLGLEPSEEAAPSPAPSE 1080  
QY 745 AGSDVFDGLGMAAGLQSLPHTDPSPLQRYSEDPTVLPSTDCGYVAPLTCSPQPEYV 804  
Db 1081 AGSDVFDGLGMAAGLQSLPHTDPSPLQRYSEDPTVLPSTDCGYVAPLTCSPQPEYV 1140  
QY 805 NQPDVFPQPPSPREGPLPAARPAATLERPKTILSPGKNGVVKDVFAGGAVENPEYLTPQ 864  
Db 1141 NQPDVFPQPPSPREGPLPAARPAATLERPKTILSPGKNGVVKDVFAGGAVENPEYLTPQ 1200

QY 865 GGAAPQPHPPAFSPAFNLVYWDODPPERGAPSTFKGTPTAENPEYLGLDVPV 919  
Db 1201 GGAAPQPHPPAFSPAFNLVYWDODPPERGAPSTFKGTPTAENPEYLGLDVPV 1255

## RESULT 12

AAU77114  
ID AAU77114 standard; Protein; 1255 AA.

XX AAU77114;

XX 05-JUN-2002 (first entry)

XX Human Her-2/neu polypeptide.

XX Human; Her-2/neu; cytostatic; haematological malignancy; CML;

KW acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL;

KW chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;

KW Hodgkin's lymphoma; T cell therapy.

XX Homo sapiens.

XX WO200213847-A2.

XX 21-FEB-2002.

XX 13-AUG-2001; 2001WO-US25408.

XX 14-AUG-2000; 2000US-0638280.

PR 28-SEP-2000; 2000US-0675904.

XX (CORI-) CORIXA CORP.

XX Gaiger A, Cheever WA, Hand-zimmermann S;

DR WPI; 2002-280741/32.

DR N-PSDB; ABK10730.

XX Inhibiting haematological malignancy development by administering polypeptide comprising immunogenic portion of Her-2/neu, polynucleotide encoding the polypeptide, or antigen presenting cells expressing the polypeptide

XX Disclosure; Page 71-74; 74pp; English.

XX The invention relates to a method for inhibiting development of

CC haematological malignancy in a patient by administering a polypeptide

CC comprising an immunogenic portion of Her-2/neu or a polynucleotide

CC encoding the polypeptide. Antigen presenting cells that express the

CC protein can also be administered. The sequences are used for inhibiting

CC development of haematological malignancy such as acute myelogenous

CC leukaemia (AML), chronic myelogenous leukaemia (CML), chronic lymphocytic

CC leukaemia (CLL), MDS, myelomas, Hodgkin's lymphoma and non-Hodgkin's

CC lymphoma. This sequence represents the human Her-2/neu polypeptide.

XX Sequence 1255 AA;

Query Match 96.5%; Score 4900; DB 23; Length 1255;

Best Local Similarity 73.2%; Pred. No. 0;

Matches 919; Conservative 0; Mismatches 0; Indels 336; Gaps 1;

QY 1 MELAALCRWGLLLALLPFGAASQVCTGTDMLRLPASPEHLDMLRHLVQGCQVVG 60

Db 1 MELAALCRWGLLLALLPFGAASQVCTGTDMLRLPASPEHLDMLRHLVQGCQVVG 60

QY 61 ELTYLPTNASLFLQDIOEVQGVLIHQNVRQVPLQRLRIRVGTQLFDNVALAVLDNG 120

Db 61 ELTYLPTNASLFLQDIOEVQGVLIHQNVRQVPLQRLRIRVGTQLFDNVALAVLDNG 120

QY 121 DPLNNTTPTVGTASPGGLRELQRLSLEILKGVLIQORNPCQYQDTILWKDIFHKNNQLA 180

Db 121 DPLNNTTPTVGTASPGGLRELQRLSLEILKGVLIQORNPCQYQDTILWKDIFHKNNQLA 180

```
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Db 181 LTLIDNRSRACHPCSPMCKGSRMGESSEDCQSLTRTVACGACRCKGPLPTDCCHEQC 240
QY 241 AAGCTGPKHSDCLACHFNHSGICELHCPALVYNTDTFESMPNPEGRYTFGASCVTACP 300
Db 241 AAGCTGPKHSDCLACHFNHSGICELHCPALVYNTDTFESMPNPEGRYTFGASCVTACP 300
QY 301 YNYLSTDVGSCTLVCPHNOEVTABDGTORCKSKPCARVCYGLGMEHLREVRVTSAN 360
Db 301 YNYLSTDVGSCTLVCPHNOEVTABDGTORCKSKPCARVCYGLGMEHLREVRVTSAN 360
QY 361 IQEFAGCKKIFGSLAPLPSFPGDPAANTAPLOPEQLQVFETLEBITGYLISAWPDSL 420
Db 361 IQEFAGCKKIFGSLAPLPSFPGDPAANTAPLOPEQLQVFETLEBITGYLISAWPDSL 420
QY 421 DLSVFQNLQVIRGRIHNGAYSILTLQGLISWGLRSRELGLALIHNNTHLCFVHTV 480
Db 421 DLSVFQNLQVIRGRIHNGAYSILTLQGLISWGLRSRELGLALIHNNTHLCFVHTV 480
QY 481 PWDQLFRPHQALLHTANRPEDECVCGEGLACHOLCARGHCWGPPTQCVCNCSQFLRGQEC 540
Db 481 PWDQLFRPHQALLHTANRPEDECVCGEGLACHOLCARGHCWGPPTQCVCNCSQFLRGQEC 540
QY 541 VEECRVLQGLPREYVYVNRHCLCHPECPQNGSVTCFGEADQCVACAHYKDPPEFCVARC 600
Db 541 VEECRVLQGLPREYVYVNRHCLCHPECPQNGSVTCFGEADQCVACAHYKDPPEFCVARC 600
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Db 601 PSGVKPDLISYMPIWKFPPDEBEGACQPCPNCTHSCVDLDDKGPAPQORASPLTS 653
QY 654 ----- 653
Db 654 ----- 653
QY 661 ILLVVVLGVVFGILIKRQOKIRKVTMRRLLOETELVEPLTPSGAMPNQAOQMRILKETEL 720
QY 654 ----- 653
Db 721 RKVKVLGSGAGTVYKGIWIPGENVKIPVALKVLRENTSPKANKEILDEAYVMAGVSP 780
QY 654 ----- 653
Db 781 YVSRLLGHICLTSTVOLVTLQMLPYGCLLDHVRNRRGLSGQDLLNWCMTAKGMSYLEDVR 840
QY 654 ----- 653
Db 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGGKVPKIMWALESLILRRFT 900
QY 654 ----- 653
Db 901 HQSDVMSYGVTVWELMTFGAKPYDGI PAREIPDLLEKGERLPQPPICTIDVYIMVVKCM 960
QY 654 ----- QNEDLPASPDLSTFVRSLLDDMDGLVDA 684
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Db 1081 AGSDVFDGDLGWAAGKIQSLPTHDPSPLOQYSEDPVTPLPSETDGYVAPLTCSPQPYV 1140
QY 805 NOPDVRPOPSPREGPLPAARPAAGATLBRPKTLPKNGVVKDVAFGCAVENPEYLTPO 864
Db 1141 NOPDVRPOPSPREGPLPAARPAAGATLBRPKTLPKNGVVKDVAFGCAVENPEYLTPO 1200
QY 865 GGAAPQHPHPPAFSPFNLYWDDPPERGAPSTFKGTATENPEYLGLDVVP 919
Db 1201 GGAAPQHPHPPAFSPFNLYWDDPPERGAPSTFKGTATENPEYLGLDVVP 1255
```

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```
RESULT 13
AAY92620
ID AAY92620 standard; Protein; 1255 AA.
XX"
AC AAY92620;
XX
DT 10-AUG-2000 (first entry)
XX
DE Human herregulin 2 (Her2).
KW Herregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity;
KW self-protein; cancer; breast cancer; prostate cancer;
KW cell-associated peptide antigen; foreign epitope.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Domain 1..173
FT /label= N-terminal
FT /note= "mature polypeptide"
FT Region 5..25
FT /label= insertion region
FT /note= "suitable for foreign epitope insertion"
FT Region 59..73
FT /label= insertion region
FT /note= "suitable for foreign epitope insertion"
FT Region 103..117
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FT /note= "suitable for foreign epitope insertion"
FT Region 149..163
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FT /note= "suitable for foreign epitope insertion"
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FT Domain 484..623
FT /label= Cysteine_rich_domain
FT Region 579..593
FT /label= insertion region
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FT /label= Transmembrane_domain
FT Region 632..652
FT /label= insertion region
FT /note= "suitable for foreign epitope insertion"
FT Region 653..667
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FT Domain 655..1010
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FT Region 661..675
FT /label= insertion region
FT /note= "suitable for foreign epitope insertion"
FT Region 695..709
FT /label= insertion region
FT /note= "suitable for foreign epitope insertion"
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Region 710..730  
 /label= insertion\_region  
 /note= "suitable for foreign epitope insertion"  
 1011..1235  
 /label= C-terminal\_domain

XX WO200020027-A2.  
 FN 13-APR-2000.  
 PD 05-OCT-1999; 99WO-DK00525.  
 XX 05-OCT-1998; 98DK-0001261.  
 PR 20-OCT-1998; 98US-0105011.  
 XX (WEBI-) M & E BIOTECH AS.  
 XX Steinaa L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;  
 PI Gautam A, Birk P, Karlsson G;  
 XX WPI; 2000-349917/30.  
 DR N-PSDB; AAA09455.  
 XX Inducing immune responses to weakly immunogenic, tumor associated  
 PT peptide antigens for the treatment of breast and prostate cancer  
 PT Claim 62; Page 193-198; 220pp; English.  
 XX This is the human heregulin 2 (Her2) sequence. Immunogenic analogues of  
 CC Her2 can be used in the claimed method as an autovaccine to induce a CTL  
 CC response. Subdominant CTL epitopes, antibody binding regions and  
 CC cysteine residues involved in disulfide bonds are preserved in the  
 CC immunogenized forms. Regions suitable for the insertion of foreign T  
 CC helper epitopes were identified (see features table). The method  
 CC is used for inducing immune responses against weakly immunogenic  
 CC cell-associated peptide antigens (PA) such as those associated with  
 CC cancers (self-proteins), e.g. human prostate specific membrane antigen  
 CC (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b).  
 CC The method comprises effecting simultaneous presentation by antigen  
 CC producing cells (APCs) of the animals immune system of: (1) at least 1  
 CC CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1  
 CC B-cell group derived from the cell-associated PA; and (2) at least 1  
 CC first T helper cell group which is foreign to the animal. Analogues of  
 CC human PSM, human Her2 and human/murine FGF8b comprising a substantial  
 CC part of all known and predicted CTL and B-cell epitopes of the respective  
 CC PA and including at least one foreign T helper epitope are also claimed.  
 CC The method is used to treat prostate, prostate/breast or breast cancer  
 CC when the PA is human PSM, FGF8b and Her2, respectively.  
 XX SQ Sequence 1255 AA;

Query Match 96.3%; Score 4892; DB 21; Length 1255;  
 Best Local Similarity 73.1%; Pred. No. 0;  
 Matches 918; Conservative 0; Mismatches 1; Indels 336; Gaps 1;

QY 1 MELAALCRWGLLALLPPGAASQVCTGTDMLRLPASPEHLDMLRLHYLQGVQVQGNL 60  
 DB 1 MELAALCRWGLLALLPPGAASQVCTGTDMLRLPASPEHLDMLRLHYLQGVQVQGNL 60  
 QY 61 ELTYLPTNASLSFLQDIQEVQGVYLIHQNQVQVPLQRLIRVRGTQLFEDNYALAVLDNG 120  
 DB 61 ELTYLPTNASLSFLQDIQEVQGVYLIHQNQVQVPLQRLIRVRGTQLFEDNYALAVLDNG 120  
 QY 121 DPLNNTTPTVGTASPGGLRELRLSLTEILKGGVLIQRNQLCYQDTILMKDIFPKNNQLA 180  
 DB 121 DPLNNTTPTVGTASPGGLRELRLSLTEILKGGVLIQRNQLCYQDTILMKDIFPKNNQLA 180  
 QY 181 LTLIDNTRGRACHPCSPMKGRCWGESSEDCQSLTRTVCAGGCARCKGKPLPTDCCHEQC 240  
 DB 181 LTLIDNTRGRACHPCSPMKGRCWGESSEDCQSLTRTVCAGGCARCKGKPLPTDCCHEQC 240  
 QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300

Db 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300  
 QY 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLRVRVTSAN 360  
 Db 301 YNYLSTDVGSCTLVCPHLNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLRVRVTSAN 360  
 QY 361 IOEFAGCKKIFGSLAFLESFDGDPASNTAPLOEQLOVFETLEITGVLYISAMPDLSL 420  
 Db 361 IOEFAGCKKIFGSLAFLESFDGDPASNTAPLOEQLOVFETLEITGVLYISAMPDLSL 420  
 QY 421 DLSVFONQVIRGRILHNGAYSLSLQGLGISWLGSLRSLRGLSLALHNNHLCFVHTV 480  
 Db 421 DLSVFONQVIRGRILHNGAYSLSLQGLGISWLGSLRSLRGLSLALHNNHLCFVHTV 480  
 QY 481 PWDQLFRNPQALLHTANRPEDECYGEGLACHQLCARGHGWPGPTQCVCNCSQFLRGQEC 540  
 Db 481 PWDQLFRNPQALLHTANRPEDECYGEGLACHQLCARGHGWPGPTQCVCNCSQFLRGQEC 540  
 QY 541 VEECRVLQGLPREYVYNAHCLPCHPECPONGSVTCFGEADQCVACAHYKDPFCVARC 600  
 Db 541 VEECRVLQGLPREYVYNAHCLPCHPECPONGSVTCFGEADQCVACAHYKDPFCVARC 600  
 QY 601 PSYKPKDLSYMPKPFDEEGACQPCINCHTSCVDLDDKGCAPARORASPLTS ----- 653  
 Db 601 PSYKPKDLSYMPKPFDEEGACQPCINCHTSCVDLDDKGCAPARORASPLTSIVSAVVG 660  
 QY 654 ----- 653  
 Db 661 ILLVVVLGVVGLILKRRQKIRKYTMRRLLQETELVEPLTPSGAMPNQAMRILKETEL 720  
 QY 654 ----- 553  
 Db 721 RKVKVLGSGAFGVYKGIWIPDGENVKIPVAIKVLRNTSPKANKEILDEAYVMAGVGP 780  
 QY 654 ----- 653  
 Db 781 YVSRLLGICLTSTVOLVTQLMPYGCLLDHVRNRRGLSQDILLNWCMTAKGMSYLEVDR 840  
 QY 654 ----- 653  
 Db 841 LVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGKVKPIKMALESILRRRT 900  
 QY 654 ----- 653  
 Db 901 HQSDVMSYGVTVWELMTFCAKPYDGIAPAREIPDLLEKGERLPPOPICTIDVYMIWKCM 960  
 QY 654 ----- QNEDIGAPASPLDSTFYRSLLLEDDDDMGDLVDA 684  
 Db 961 IDSECRPRRELVSFSEFMRWDPQRFVVIQNEEDLGPASPLDSTFYRSLLLEDDDDMGDLVDA 1020  
 QY 685 EBYLVPQOQFFCPDPAPGAGVMVHRHRSSTRSGGDLTLGLEPSEEBAPRSLAPSEG 744  
 Db 1021 EBYLVPQOQFFCPDPAPGAGVMVHRHRSSTRSGGDLTLGLEPSEEBAPRSLAPSEG 1080  
 QY 745 AGSDVDFDGLGMAAKGLQSLPHTDPSPLQRYSEBPTVPLPSETDGYVAPLTCSPQEV 804  
 Db 1081 AGSDVDFDGLGMAAKGLQSLPHTDPSPLQRYSEBPTVPLPSETDGYVAPLTCSPQEV 1140  
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 Db 1141 NOPDYRPPQPPSPREGPLPAARAGATLERPKTSLPGKNGVVDVAFGGAIVENPEYLTQ 1200  
 QY 865 GGAAPQPPPPAFSPAFNLYYWDQPPPERGAPSTFKGTPTAENPEYLGLDVFPV 919  
 Db 1201 GGAAPQPPPPAFSPAFNLYYWDQPPPERGAPSTFKGTPTAENPEYLGLDVFPV 1255

RESULT 14  
 AAEL12130  
 ID AAEL12130 standard; Protein; 1255 AA.  
 XX  
 AC AAEL12130;  
 XX

DT 18-DEC-2001 (first entry)  
 DE Human tyrosine kinase-type receptor, HER-2.  
 XX  
 KW Therapeutic compound; major histocompatibility complex; vaccine;  
 KW antigenic peptide; MHC; immunoregulatory; immune response; HER-2;  
 KW adoptive immunotherapy; anti-cancer; breast cancer antigen; APC;  
 KW antigen presenting cell; human; tyrosine kinase-type receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 774..782  
 FT /note= "Antigenic epitope"  
 XX  
 PN WO200168677-A2.  
 XX  
 PD 20-SEP-2001.  
 XX  
 PF 16-MAR-2001; 2001WO-US40328.  
 XX  
 PR 16-MAR-2000; 2000US-0527487.  
 XX  
 PA (GENZ ) GENZYME CORP.  
 XX  
 PI Nicolette CA;  
 XX  
 DR WPI; 2001-616284/71.  
 DR N-PSDB; RAD19731.  
 XX  
 PT Novel synthetic therapeutic compound for inducing immune response and  
 PT for use in adoptive immunotherapy, has enhanced binding to major  
 PT histocompatibility molecules and enhanced immunoregulatory properties  
 PT  
 XX  
 PS Claim 4; Page 63-67; 69pp; English.  
 XX  
 CC The invention relates to synthetic therapeutic compounds (antigenic  
 CC peptides) with enhanced binding to major histocompatibility complex  
 CC (MHC) molecules and enhanced immunoregulatory properties relative  
 CC to their natural counterparts. Compounds of the invention are useful  
 CC for inducing an immune response in a subject and for use in adoptive  
 CC immunotherapy. They are useful as components of anti-cancer vaccines  
 CC and to expand immune effector cells that are specific for cancers  
 CC characterised by expression of the breast cancer antigen, HER-2.  
 CC Polynucleotides that encode peptides of the invention are useful as  
 CC hybridisation probes and as primers for the detection of genes of gene  
 CC transcripts that are expressed in antigen presenting cells (APCs), to  
 CC confirm transduction of polynucleotides into host cells. The present  
 CC sequence is human tyrosine kinase-type receptor, HER-2. Compounds  
 CC of the invention are designed based on the HER-2 antigenic peptide  
 CC (774-782).  
 XX  
 SQ Sequence 1255 AA;  
 Query Match 96.3%; Score 4892; DB 22; Length 1255;  
 Best Local Similarity 73.1%; Pred. No. 0;  
 Matches 918; Conservative 0; Mismatches 1; Indels 336; Gaps 1;  
 QY 1 MELAAACRWGLLALLPFGAASQVCTGDMKRLPASPETHLMRLHYGCGVQGNL 60  
 DB 1 MELAAACRWGLLALLPFGAASQVCTGDMKRLPASPETHLMRLHYGCGVQGNL 60  
 QY 61 ELTYLPTNASLFLDIOEGVYLIHNOVROVPLQRLVRGTQLFEDNYALVLDNG 120  
 DB 61 ELTYLPTNASLFLDIOEGVYLIHNOVROVPLQRLVRGTQLFEDNYALVLDNG 120  
 QY 121 DPLNNTTVPVTCASPGGLRELQRLSLTEILKGVLIQRPOLCYQDTILWKDIFHKNQOLA 180  
 DB 121 DPLNNTTVPVTCASPGGLRELQRLSLTEILKGVLIQRPOLCYQDTILWKDIFHKNQOLA 180  
 QY 181 LTLIDTNRSRACHPCSPMKGSRGWGESSEDCQSLTRTVAGGCARCKGPIPTDCCHQC 240

RESULT 15  
 AAB60167

Db 181 LTLIDTNRSRACHPCSPMKGSRGWGESSEDCQSLTRTVAGGCARCKGPIPTDCCHQC 240  
 QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300  
 Db 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300  
 QY 301 YNYLSTDVGSCTLVCPHNVHTAEDGTORCEKSKPCARVCYGLGMEHLREAVTTSAN 360  
 Db 301 YNYLSTDVGSCTLVCPHNVHTAEDGTORCEKSKPCARVCYGLGMEHLREAVTTSAN 360  
 QY 361 IOEFAGCKKIFGSLAFIPESPDGPASNTAPLQPEQLQVFTTEITGYLYISAMPDLSL 420  
 Db 361 IOEFAGCKKIFGSLAFIPESPDGPASNTAPLQPEQLQVFTTEITGYLYISAMPDLSL 420  
 QY 421 DLSVFQNLQVIRGRILHNGAYSLTQGLIGISWGLSLRELGLALIHNTLHLCFVHTV 480  
 Db 421 DLSVFQNLQVIRGRILHNGAYSLTQGLIGISWGLSLRELGLALIHNTLHLCFVHTV 480  
 QY 481 PWDQLFRNPHOALLHTANRPEDECVGEGGLACHQICARGHCWGPPTQCVNCSQFLRGQEC 540  
 Db 481 PWDQLFRNPHOALLHTANRPEDECVGEGGLACHQICARGHCWGPPTQCVNCSQFLRGQEC 540  
 QY 541 VEECRVLQGLPREYVYNAHCLPCHPECOPOGNSVTCFGEADQCVACAHYKDPPECVARC 600  
 Db 541 VEECRVLQGLPREYVYNAHCLPCHPECOPOGNSVTCFGEADQCVACAHYKDPPECVARC 600  
 QY 601 PSGVKPDLSTYMPIWKFPDEGACQPCPINCTHSCVDLDDKGCPAEQASPLTS ----- 653  
 Db 601 PSGVKPDLSTYMPIWKFPDEGACQPCPINCTHSCVDLDDKGCPAEQASPLTSIVSAVVG 660  
 QY 654 ----- 653  
 Db 661 ILLVVLGVVFGIILIKRRQKIRKYTWRRLLQETELVEPLTPSGAMPNQAMRILKETEL 720  
 QY 654 ----- 653  
 Db 721 RKVKVLSGAFGTVYKGIWIPDGENVKIPVAIKVLRNTPSKANKEILDEAYVMAGVSP 780  
 QY 654 ----- 653  
 Db 781 YVSRLLGICLTSTVQLTQMPYCLLDHVNRGRGLSQDLLNWCQIAKGMVLEVDVR 840  
 QY 654 ----- 653  
 Db 841 LVHRDLAARNVLKSPNHVKITDFGLARLLIDETEHADGKVPKIMMALESILRRFT 900  
 QY 654 ----- 653  
 Db 901 HQSDVWSYGVTVWELMTFGAKPYDGI PAREIPDLLEKGERLPQPICTIDYVIMVWKCM 960  
 QY 654 -----QNEIDLGPAFLDSTFYRSLLDDDDMDGLVDA 684  
 Db 961 IDSECRPRFRELNVSEFSRMARDPQRFVVIQNEIDLGPAFLDSTFYRSLLDDDDMDGLVDA 1020  
 QY 685 EYLVLPQGGFFCPDPAPCAGGMVHHRSSSTRSGGDLTLGLPFSSEAPRSLAPSEG 744  
 Db 1021 EYLVLPQGGFFCPDPAPCAGGMVHHRSSSTRSGGDLTLGLPFSSEAPRSLAPSEG 1080  
 QY 745 AGSDVFDGLGMAAGKGLQSLPHTDPSLQRYSEDPTVLPSETDGYVAPLTCSPQPEYV 804  
 Db 1081 AGSDVFDGLGMAAGKGLQSLPHTDPSLQRYSEDPTVLPSETDGYVAPLTCSPQPEYV 1140  
 QY 805 NOPDVRPQPPSPREGPLPAARPAAGATLERPKTLSPGKNGVVKDVFAGGAVENPEYLTPO 864  
 Db 1141 NOPDVRPQPPSPREGPLPAARPAAGATLERAKTLSPGKNGVVKDVFAGGAVENPEYLTPO 1200  
 QY 865 GGAAAPQHPPPAFSPFDNLYYWDQDPPERGAPSTFKGTPTAENPEYLGDDVPV 919  
 Db 1201 GGAAAPQHPPPAFSPFDNLYYWDQDPPERGAPSTFKGTPTAENPEYLGDDVPV 1255

ID AAB60167 standard; Protein; 1255 AA.  
XX AAB60167;  
AC AAB60167;  
XX 03-APR-2001 (first entry)  
DT HER2 transgene plasmid construct encoded protein.  
DE  
XX  
XX  
KW Human; HER2; ErbB2 receptor; p185neu; maytansinoid conjugate; cancer;  
KW antibody.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX  
XX WO200100244-A2.  
XX  
XX  
XX 04-JAN-2001.  
XX  
XX 23-JUN-2000; 2000WO-US17229.  
XX  
XX 25-JUN-1999; 99US-0141316.  
XX 16-MAR-2000; 2000US-0189844.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Erickson S, Schwall R;  
XX  
XX WPI; 2001-061962/07.  
XX N-PSDB; AAF24297.  
XX  
XX  
XX Treating tumors, particularly breast cancers, which overexpress an ErbB  
PT receptor and does not respond to an anti-ErbB antibody, comprises  
PT conjugating the antibody to a maytansinoid -  
XX  
XX Example 3; Fig 4; 92pp; English.  
XX  
XX The present invention provides a method of treating cancer by  
CC administering a conjugate of anti-ErbB antibody with a maytansinoid. In  
CC particular, the antibody is directed against ErbB2 (also known as HER2  
CC and p185neu). The method is particularly useful in the treatment of  
CC breast, ovarian, stomach, endometrial, salivary gland, lung, kidney,  
CC colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.  
XX  
XX Sequence 1255 AA;  
XX  
Query Match 96.3%; Score 4892; DB 22; Length 1255;  
Best Local Similarity 73.1%; Pred. No. 0;  
Matches 918; Conservative 0; Mismatches 1; Indels 336; Gaps 1;  
QY 1 MELAALCRWGLLMLALLPPGAASQVCTGTDMLRLPASPEHLDMRLHLYQGCVVQGNL 60  
DB 1 MELAALCRWGLLMLALLPPGAASQVCTGTDMLRLPASPEHLDMRLHLYQGCVVQGNL 60  
QY 61 ELTYLPTNASLSPLQDIOEVQGVVLIHQNQVQVPLQRLIRVGTQLPEDNVALAVLDNG 120  
DB 61 ELTYLPTNASLSPLQDIOEVQGVVLIHQNQVQVPLQRLIRVGTQLPEDNVALAVLDNG 120  
QY 121 DPLNNTPTVGTASPGGLRELQRLSLTEILKGGVLIQRLNQLCVDPTILMKDIFHKNQOLA 180  
DB 121 DPLNNTPTVGTASPGGLRELQRLSLTEILKGGVLIQRLNQLCVDPTILMKDIFHKNQOLA 180  
QY 181 LTLIDNTRGRACHPCSPMKGSRGWESSEDCOSLRTVTCAGGACRCKGLPTDCCHEQC 240  
DB 181 LTLIDNTRGRACHPCSPMKGSRGWESSEDCOSLRTVTCAGGACRCKGLPTDCCHEQC 240  
QY 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300  
DB 241 AAGCTGPKHSDCLACLFHNSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300  
QY 301 YNYLSTDVGSCTLVCPHLNQEVTAEDTORCEKSPKPCARVCYGLGMEHLREVAVTSAN 360  
DB 301 YNYLSTDVGSCTLVCPHLNQEVTAEDTORCEKSPKPCARVCYGLGMEHLREVAVTSAN 360

QY 361 IOEFAGCKKIFGSLAFLEPESFDGDPASNTAPLQEPQLOVFETLEBITGYLYISAMPDLSLP 420  
DB IOEFAGCKKIFGSLAFLEPESFDGDPASNTAPLQEPQLOVFETLEBITGYLYISAMPDLSLP 420  
QY 421 DLSVFONLOVIRGRILHNGAYSLTQGLGISWLGURSRELGSGLALIHNTHLFCFVHTV 480  
DB DLSVFONLOVIRGRILHNGAYSLTQGLGISWLGURSRELGSGLALIHNTHLFCFVHTV 480  
QY 481 PWDQLFRNPHOALLHTANRPEDECYEGGLACHQLCARGHCWGPPTQCVCNCSQFLRGQBC 540  
DB PWDQLFRNPHOALLHTANRPEDECYEGGLACHQLCARGHCWGPPTQCVCNCSQFLRGQBC 540  
QY 541 VEECRVLQGLPREYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKDPDFCVARC 600  
DB VEECRVLQGLPREYVNAHCLPCHPECPQNGSVTCFGEADQCVACAHYKDPDFCVARC 600  
QY 601 PSGVKPDLSPYMPKPFDEEGACQPCINCHTHSCVDLDDKGCPCAFORASPLTS----- 653  
DB PSGVKPDLSPYMPKPFDEEGACQPCINCHTHSCVDLDDKGCPCAFORASPLTS----- 653  
QY 654 ----- 653  
DB 661 ILLVVVLGVVFGILLIKRRQOKIRKYTMERLLQETELVEPLTPSGAMPNQAOQMRILKETEL 720  
QY 654 ----- 653  
DB 721 RKVKVLGSGAGTVYKGIWIPDGENVKIPVAIKVLRNTPSKANKEILDEAYVMAGVGP 780  
QY 654 ----- 653  
DB 781 YVSRLLGLCTSTVOLVTQMPYGLDHLVRENRRGLSGDQLLNMCMQIAKMSYLEVVR 840  
QY 654 ----- 653  
DB 841 LVHRDLAARNVLVSPNHVKITDFGLARLLDIDETEHADGCKVKPIKMALESILRRRT 900  
QY 654 ----- 653  
DB 901 HQSDVMSYGVTVWELMTFGAKPYDGI PAEIPDLLEKGERLPQPPICTIDVYMIVMVKWM 960  
QY 654 -----ONEDLGPASPLDSTFYRSLLLEDDMDGLVDA 684  
DB 961 IDSECRPRFRLVSEFSRMARDPQRFVVIQNEDELGPASPLDSTFYRSLLLEDDMDGLVDA 1020  
QY 685 REYLVPOQGFCDPAPGAGGMVHHRSSSTRSGGDLTLGLEPSEEEAPRSLAPSEG 744  
DB 1021 REYLVPOQGFCDPAPGAGGMVHHRSSSTRSGGDLTLGLEPSEEEAPRSLAPSEG 1080  
QY 745 AGSDVFDGDLGMAAKGLQSLPTHDPSPLQRYSEDPVPLPSETDGYVAPLTCSPQETV 804  
DB 1081 AGSDVFDGDLGMAAKGLQSLPTHDPSPLQRYSEDPVPLPSETDGYVAPLTCSPQETV 1140  
QY 805 NOPDVRRPQPPSPREGPLPAARPAAGATLERPKTLPKNGVVKDVFAFGAVENPEYLTQ 864  
DB 1141 NOPDVRRPQPPSPREGPLPAARPAAGATLERPKTLPKNGVVKDVFAFGAVENPEYLTQ 1200  
QY 865 GGAAAPQHPPPAFSPAFNLYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVVP 919  
DB 1201 GGAAAPQHPPPAFSPAFNLYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVVP 1255

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Job time : 59.6401 secs